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I bases I to 1440)
Thomas, W. J. Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuchihashi, Z. and Wolff, R.K.
Hereditary hemochromatosis gene products
Fatent: US 6140305-A 9 31-OCT-2000;
Focation Control 
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ACCESSION
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AUTHORS
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FEATURES
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AR117793
LOCUS
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Db 1021 GGATAACCTTGGCTGTACCCCCTG Qy 1081 CAGGCCTGATCGCCCCATTG Db 1081 CAGGCCTGATCAGCCCCTATTG Db 1081 TTGGAGTCATCAGCCCCTATTG Qy 1141 TTGGAGTCATCAGTGGAATTGCTG Qy 1201 TAATATAAGGAAGAGAATTCCTG Qy 1201 TAATATAAGGAAGAGCAGGTT Db 1201 TAATATAAGGAAGAGCAGGTT CHIHIHIHID Db 1261 GTGAGTGACACCCAGCCTGCAGACT QY 1261 GTGAGTGACAGCCAGCCTTG QY 1261 GTGAGTGACAGCCAGCCTGCAGACT QY 1261 GTGAGTGACACCCAGCCTGCAGACT CO 13321 AGGAGTGCATTATGAGCAGCCTCCTCG	GGGAGTGCATTATGAG GCCTGACGAACTCCTTG 	ITTION SION ON RDS ED ANISM ENCE HORS	hemochromatosis gene Patent: US 6228594-A 10.000 Coation/Qua 10.1440 Proganism="u 347 a 355 c 355 c 100.08;	Matches 1 1 61	Oy 121 CCTAGGCATAGGTGTAGGTGACC 11111111111111111111111111111111111
### Best Local Similarity 100.0%; Pred. No. 0; ###################################	11	421 GTGTGGAGCCCGGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	541 601 601 661 661		901 CCTTGAACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGG 960
		64 B 64 64 64 64 64 64 64 64 64 64 64 64 64	o d a d d d	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	04 B O4

ö PAT 08-AUG-2001 GTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCA 1140 1200 TCAAGAGGAGCCATGGGCACTACGTCTTAGCTGAAC 1260 AGCCTTCTCTGTTCATTTCCTCAAAAGATTTCCCCA 1440 GGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACC 1080 GTTTTTGTCGTCATCTTGTTCATTGGAATTTTGTTCA 1200 CATGITICAGGAGAGAGITGAACCIAAACAIAGAAAI 1380 D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
liff, R.K.

19 the presence or absence of a hereditary
mitation
9 08 MAY-2001;
liffers 240 CTTCTGGAGCCATCCCCGTTTCCCCGGCCCCCAAAG 180 Gaps TTCACAAGCAGGTACCTTCTGCTGTAGGAGAGAGA 60 GCGGCCAGAGCTGGGGAAATGGGCCCGCGAGCCAGGC GCGCCCAGAGCTGGGGAAATGGGCCCGCGAGGCCAGGC ö Score 1440; DB 6; Length 1440; Pred. No. 0; 0; Mismatches 0; Indels 0; linear DNA Ų 331 1440 bp t US 6228594. unknown" 407 g 54

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CACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGT 	TGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCC 	GTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGGCTGCAGC 	GAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGG 	AAAATCACAACACACAGGAGGTCCCACACCTGCAGGTCATCCTGGGCTGTGAAATGC 	AAGAACACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGGCAGGACCACCTTG	AATTCTGCCCTGACACACTGGATTGGAGAGCAGGAGCGGAGGCCTGGCCCACGAGGCIIIIIIIIII	GGAGTGGCAAAGCCACAAGATTCGGGCCAGGCAGAGAGGGCCTACCTGGAGAGGGACT 	GCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTTTTGGACCAACAAGTGC 	CTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGG 	CTTGAACTACTACCCCGGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGG 	ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCT 	GATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACCCCCCCC	CAGGCCTGGATCAGCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCTAGTCA :	TGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTGTTCA 	TAATATTAAGGAAGAGGAGGGTTCAAGAGGAGCCATGGGGGACTACGTCTTAGCTGAAC : 	GTGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGAAAAACTAGAGACTCAAAG : 	SGAGTGCATTTATGAGGTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAAT
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QY	Qy Db	Qy	Qy Db	Qy	QY.	QY	Qy Db	Oy Db	Qy Dp	QY	Qy Dp	Oy Dp	Qy Qp	Qy	Qy Db	Qy Db	Qy Db

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HSU60319 2727 bp mRNA linear PRI 29-OCT-1997
Homo sapiens haemochromatosis protein (HLA-H) mRNA, complete cds.
U60319
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/db_xref="id="haC51823.1"
/translation="haCPRARPAILLIAMILQTAVLOGRILRSHSLHYLEMGASEQDLGL
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RAMPTKLEWERHKIRARQNRAYLERDCPAQLQCLELGRGVLDQQVPPLWYTTRORALNYYPQNITMKWMLEDKQPMDAKEFEPRNYLPUSGSVYTLRCRALNYYPQNITMKWMLEDKQPMDAKEFEPRNYLPUSGSVYQGWITLAVPPPGE
SPRTGQQVPLHOLDQPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFIILRKRQG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2727)
Feder,J.N., Gnirke,A., Thomas,W., Tsuchihashi,Z., Ruddy,D.A.,
Basava,A., Dormishian,F., Doningo,R., Ellis,M.C., Fullan,A.,
Hinton,L.M., Jones,N.L., Kimmel,B.E., Krommal,G.S., Lauer,P.,
Lee,V.K., Loeb,D.B., Mapa,F., McClelland,E., Meyer,N.C.,
Mintier,G.A., Mooeller,N., Moore,T., Morkang,E., Frass,C.E.,
Quintana,L., Stranes,S. M., Schatzman,R.C., Brunke,K.J.,
Drayna,D.T., Risch,N.J., Bacon,B.R. and Wolff,R.K.
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L. Submitted (10-JUN-1996) Mercator Genetics, 4040 Campbell Ave., Menlo Park, CA 94025, USA
Menlo Park, CA 94025, USA
Menlo Park, CA 1277
Gaps
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/gene="HLA-H"
/codon_start=1
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/note="HFE"
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361 361	TTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCTATGATCATGAGAGTCGCC 420
421	GIGIGGAGCCCGAACTCCAIGGITTCCAGIAGAAITICAAGCCAGAIGIGGCIGCAGC 480
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541 541	AAAATCACAACCACAGGAGGCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGC 600
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661 661	AATICTGCCCTGACACACAGGATTGGAGGGGGGGGGGGGG
721	TGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGCCTACCTGGAGAGGACT 780
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841 841	CTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGG 900
901	CCTIGAACTACTCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGG 960
961 961	ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCT 1020
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081 081	CAGGCCTGGATCAGCCCTCATTGTGATCTGGGAGCCCTCACCGCCTGGCACCCTAGTCA 1140
141	TIGGAGICAICAGIGGAATIGCTGITITIGICGICAICTIGITCATIGGAATITIGITCA 1200

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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 10 31-0CT-2000;
Location/Qualifiers
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Pred. No. 0;
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Sequence 10 from patent US 6140305.
AR117794 GI:14098700
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Pred. No. 0;
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Thomas,W.J., Drayna,D.T., Feder,J.N.
Tsucchinashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene prod
Patent: US 6140305-A 11 31-OCT-2000;
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  6140305
                                                                                                                           Location/Qualifiers
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Sequence 11 from patent
                      GI:14098701
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Best Local Similarity 99.99
Matches 1439; Conservative
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Thomas,W.J., Drayna,D.T., Feder,J.N.,
Tsuchihashi,Z. and Wolff,R.K.
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Method for determining the presence or hemochromatosis gene mutation
Patent: US 622894-A 11 08-MAX-2001;
Location/Qualifiers
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         CTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGG
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AATTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGGGCCTGGCCCACCAAGC
                                                                              GCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGGTGTTTTGGACCAACAAGTGC
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Thomas,W.J., Drayna,D.T., Feder,J.N., 'Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or hemochromatosis gene mutation
Patent: US 6228594-A 12 08-MAY-2001;
Location/Qualifiers
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AR149466.1 GI:15114057
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                                                                                                                      Unclassified.

1 (bases 1 to 1440)

1 (bases 1 to 1440)

Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D. Tsuchihashi, Z. and Wolff, R.K.

Hereditary hemochromatosis gene products

Patent: US 6140305-A 12 31-0CT-2000;
                                                                                                                                                                                                                                                          Length 1440;
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0; Mismatches
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US 6140305
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1. .1440
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354 c 407 a
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                                                                               AR117796.1 GI:14098702
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99.9%;
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Matches 1438; Conservative
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/evidence-experimental
/product="hemochromatosis protein"
/protein_id="cAc67792.1"
/pbctein_id="cA6419"
/translation="MGPRARPALLLLMLLQTAVLQGRLLPLGYVDDQLFVFYDHESRR
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Submitted (06-SEP-1999) Oliva R., Faculty of Medicine and Clinic Submitted (06-SEP-1999) Oliva R., Faculty of Medicine and Clinic Hospital, Human Genome Research Group, Casanova 143, 08036, SPAIN Location/Qualifiers
1. 1280
/organism="Homo sapiens"
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Oliva, R. and Sanchez, M. Identification of different alternative splicing forms of the HFE
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                                           GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGATATACGTACCAGGTGGAGCACC
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AJ249335.1 GI:15485418
alternative splicing; hemochromatosis protein; HFE gene.
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/chromosome="6"
/map="6p22"
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161. 1138
/gene="HFE"
161. .1138
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2 (bases 1 to 1280)
Oliva, R.
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ENCPAALGOGLLELGRGVLDQQVPPLVKVTHHYTSSYTTLRCRALNYYPGNITWKWLK
DKQPWDAKEFEPROVLPNGGTYQGMITLAVPPGEEQRYTCQVEHPGLDQPLIVIWEP
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termination variant terE6 (HFE) mRNA,
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Aboxref="G1:11094315"
/translation="WERRARPALLILMILOTAVLOGRILRSHSLHYLEMGASEODIGL
SLFEALGYVDDQLFVFYDHESRRVEPFTPWVSSRISSQMWLQLSQSLKGWDHMFTVDF
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1 (bases 1 to 1200)
Thenle,A., Orhant,M., Gicquel,I., Fergelot,P., Le Gall,J.Y., David,V. and Mosser,J.
The HFE gene undergoes alternate splicing processes
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            GATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACCC
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Direct Submission
Submitted (17-DEC-1998) UPR 41 CNRS, Fa
Pr. Bernard, Rennes 35043, France
1. 1200
Arganism="Homo sapiens"
Ab zref="texon:9606"
Arganism="Homo sapiens"
Ab zref="texon:9606"
Arganism="Homo sapiens"
Ab zref="texon:9606"
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SVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYGGWITLAVPPGE
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                                                                                                                                                                 CCGCGGTCCTGCAGGGGCGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTG 330
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                                                                                                                                                                                                                                                                                                                                      CCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGA
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                                                                                      82.6%; Score 1189; Clarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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Best Local Similarity
Matches 1189; Conserv
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(HFE) mRNA,
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GAGCCATGGGGCACTACGTCTTAGCTGAACGTGACACGCAGCCTGCAGACTCACTG
                                                                                                                                                                       GAGATITIAACGGGGACGTGCGGCCAGAGCTGGGGAAATGGGCCCGCGAGCCAGGCCGGGCG
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Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1045;
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AP079407
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Pred. No. 2.7e-280;
); Mismatches 0;
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Rhodes, D.A.
Direct Submission
Submitted (21-JJL-1998) Immunology, Un.
Court Road, Cambridge CB2 1QP, UK
Location/Qualifiers
1. .1045
//organism="Homo sapiens"
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//mnp=_fp22.1"
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Mammalia, Eutheria, Primates,
1 (bases 1 to 1045)
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RALTTKLEWEVNKIRAKQNRAYLERDCPEDLGWLLELGRGYLDQOVPPLVKYTHHVAS
RALTTKCOVEHPGLDOPLTATWEPSLSNTLYGVISGIAVCVIIFFIGILFRILRRROBG
SORYTCOVEHPGLDOPLTATWEPSLSNTLYTGVISGIAVCVIIFFIGILFRILRRROBG
SRGAMGDYVLGECE"
                                                        22-OCT-2000
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium. I (bases 1 to 1320)
West, C.J., Worley, M. and Beutler, E. Rhinoceros HFE Polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 AGGGTGACTTCTGGAGCCATCCCCGTTTTCCCCGCCCCCAAAAGAAGCAGAGTTTAACG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                Unpublished

2 (bases 1 to 1320)
West,C.J., Worley,M. and Beutler,E.
Direct Submission
Submitted (29-AUG-2000) Molecular and Experimental Medicine,
Scripps Research Institute, 10550 North Torrey Pines Road, La
Jolla, CA 92037, USA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AGCACCCGGGGTCCGAGCCGGGGAAATGGGCCCGCGGGGCCCGAGCCCGCGCTCTTCTTCCT
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mRNA, complete cds
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Best Local Similarity 82.4%; Pred. No. 4.5e-252;
Matches 1065; Conservative 0; Mismatches 225;
                                                                                                                                                                                                                                                                                                                            /organism="Ceratotherium simum"
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86. .1132
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simum HFE protein
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TGACACG 1045
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AUTHORS
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                                                                                                              2 (bases 1 to 1320)
West, C.J., Worley, M. and Beutler, E.
Direct Submission
Submitted (29-AUG-2000) Molecular and Experimental Medicine,
Scripps Research Institute, 10550 North Torrey Pines Road, La
Jolla, CA 92037, USA
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Mammalia; Eutheria; Perissodactyla; Rhinocerotidae;
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0; Mismatches 225; Indels
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West,C.J., Worley,M. and Beutler,E.
Rhinoceros HFE Polymorphisms
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                                                      CAAGGAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTAC
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797 6	GCAGTTGCTGGAGCTGGGGAGAGGTGTTTTGGACCAACAGTGCCTCCTTTGGTGAGGT 856		
857 G	GACACATCATGAGCCTCTTCAGTGACCACTCTACGGTGTGGGCCTTGAACTACCC 916 		
917 0	CCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGTGGATGCCAAGGAGTTCGA 976 	BASE CORIGIN	BASE COUNT ORIGIN
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1157 #	1157 AATTGCTGTTTTTGTCGTCATCTTGTTCGAATTTTGTTCATAATATTAAGGAAGAG 1216 	oy Qy	61 AGC 257 GAT
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1337 #	AGCTCTTCATGTTTCAGGAGAGTTGAACCTAA-ACATAGAAATTGCCTGACGAACTCC 1395 	oy Oy	
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RESULT 15 AY007544 LOCUS		g o	
DEFINITION ACCESSION VERSION KEYWODDS	Rhinoceros unicornis HFE protein mRNA, complete cds. AY007544 AY007544.1 GI:10945693	oy d	617 CGA
ORGANISM	Greater Indian rhinoceros. Rhinoceros unicornis Bukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	oy Oy	
REFERENCE AUTHORS		Dp Oy	541 ACT 737 CAA
TITLE JOURNAL	Rhinoceros HFE Polymorphisms Unpublished 1990	qa	601 CAA
FERENCE AUTHORS TITLE	<pre>/ Unsers I to 1319) West,C.J., Worley,M. and Beutler,E. Direct Submission</pre>	Qy	797 GCA
JOURNAL	Submitted (29-AUG-2000) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 North Torrey Pines Road, La	qq	
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Jolla, CA 92037, USA

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llarity 81.9%; Pred. No. 5.1e-252;
Conservative 0; Mismatches 232;
                       unicornis
               /organism="Rhinoceros
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901 GCCCCCGGGGAAGAGCAGAGATATACCTGCCAGGTGGAGCACCAGGCCTGGATCAGCC
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Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June 19, 2002, 06:38:34 ; Search time 2546.54 Seconds (without alignments) 7632.166 Million cell updates/sec Run on:

US-09-497-957-9 1440 1 GGGGACACTGGATCACCTAG......TCCTCAAAAAGATTTCCCCA 1440 Perfect score: Sednence: Title:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ф	Query	51.3	44.0	35.2	24.9	19.7	19.2	18.0	17.5	17.2	16.1	15.7	14.9	14.7	14.2	13.8	13.8	13.0
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/db_xref="taxon:9606"
/dlone="TMAGE:4857941"
/clone="TMAGE:4857941"
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/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)" /ite_lost="Organ: colon; Vector: pOTB7; Site_l: Xho1; Site_2: ECOR1; cDNA made by oligo-df priming. Directionally cloned into ECOR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in

B 174 12.1 394 10 BF4664345 9 170.4 11.8 444 12 AZ025590 0 160 11.1 334 9 AW902003 1 156.8 10.9 536 12 AZ074871 2 154 10.7 805 10 BG402460 3 153.6 10.7 1016 9 AL532717	24 151.8 10.5 289 10 H33444 H3544 EST109830 R 25 151.6 10.5 481 12 AZ025784 AZ025784 AZ025784 REC123-3 26 145.6 10.1 1031 9 AL513728 AL541209 AL541209	BG747345 BG747345 BG747345 BG747345 BG747345 BG747345 BG747345.1 GI:14057998	NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/. Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laborator CDNA Library Preparation: Ling Hong/Rubin Laborator CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution informat found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Plate: LLCM711 row: d column: 06	High quality sequence sto Location/Qualifi
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BASE COUNT ORIGIN

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Mammalia; Eutheria; Rodentia;
                                    trapper.
                                                                                         clone:2310032M04.
                                                                                                          Mus musculus
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the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)" 201 c 235 g 181 t
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Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310032M04:hemochromatosis, full insert sequence.
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                                                                                                                                                                                                     384 GACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGGAGCCCCGGACTCCATGG 443
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                                                                                                                                                                    Gaps
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                                                                                                                                                                  3,
                                                                                                                              Length 819;
                                                                                                                              Score 738.6; DB 10; Length
Pred. No. 2.2e-194;
0; Mismatches 29; Indels
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al Similarity 96.1%;
789; Conservative
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RESULT 2 AK009581 LOCUS DEFINITION

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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

Chases I to 1723)

Rackway, I to 1723)

Rackway, I saladarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukuda, Y., Burono, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishli, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Koda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Soltimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Tasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Submitted (10-701-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Riken Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Ronno,H., Akiyama,J., Nishi,K., Kitaunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yamamoto,R., Trouch,K., Togawa,Y., Izawa,M., Ohara,E., Warahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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The RIKEN Genome Exploration Research Group Phase II Team and
Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                           Carninci,p. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/db_xref="G1:12844463"
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/dev_stage="adult"
99. .1178
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Pred. No. 4.6e-165
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                                                                                                                                                                                            /strain="C57BL/6J"
/db.xref="MGD:MGI:1905246"
/db.xref="Taxon:10090"
/clone="2310032M04"
/sex="male"
                                                                                                  with XhoI and SstI. Cloning sites,
Host: SOLR.
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/organism="Mus musculus"
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BEZ72926 570 bp mRNA linear EST 13-JUL-2000 601171213F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3544803 5', mRNA sequence.
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                                                                                       GATTGGAGGGAGCAGCAGAACCCAGGGCCTGGCCCAAGCTGGAGTGGGAAAGGCACAAG 740
                                                                                                                                                                                                                                                                                                                                                  ATTCGGGCCAGGCAGAACAGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCAG 800
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                                                              TTCTGGACTATTATGGAAAATCACAACCACAGCAAG--
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1.384
/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Ab_xref="taxon:966"
/ Clone_lib="Er0209"
/ Gerives stage="Adult"
/ Anote="Organ: lung_tumor; Vector: puc18; Site_1: Sma1;
/ Anote="Organ: lung_tumor; Vector was made by cloning products Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PRR (U.S. Letters Patent application No. 196,716 - Luding Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 38).
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,A., da Silva,W. Jr., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Matsukuma,A., Baia,G.S., Simpson,D.H., W.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Tel: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Thtp://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-ET0209-151200-003-f07&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                              BF883952
PM4-EI0209-151200-003-f07 ET0209 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Shorgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
979 CTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTAC 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 ACCAGCTGTTCTGTTCTATGATCATGAGAGTCGCCGTGTGGGAGCCCCGAACTCCATGGG 444
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High quality sequence stop: 384.
Location/Qualifiers
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BF883952.1 GI:12274078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      739 AGATICGGGCCAGGCAGAACAGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGG 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           799 AGTTGCTGGAGCTGGGGAGAGGTGTTTTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGA 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          560 GGAGICCCACACCCIGCAGGICATCCIGGGCIGIGAAAIGCAAGAAGACAACAGTACCGA 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.2%; Score 506.8; DB 10; Best Local Similarity 99.4%; Pred. No. 6.3e-130; Matches 519; Conservative 0; Mismatches 2; I
                        GI:9147279
                                                                           Homo sapiens
        BE272926
BE272926.1
                                                           human.
                                                                                                                                                                                                                                                                                                                                                                            source
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ORIGIN
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AUTHORS
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        ACCESSION
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KEYWORDS
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Design and use of two pooled tissue normalized CDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
For 16, Clay Center, NE 68933-0166, USA
Fal: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Smail: Smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 523)
2 Eshrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, N.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
             GTGACTICTGGAGCCATCCCCGTTTCCCCGCCCCCCAAAAGAAGCGGAGATTTAACGGGG 199
                                                                                                                                                  114 CCTCCTGCGGGACCGTGGCCACGCGGGGCGCGCGCGCACACTCCCTGCTTTCCT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGATGACCAGCTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCCGAACTCC 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 CTGGCTCTCGGGTAAGGCCTCCAACCAACTGTGGCTGCAGCTAAGCCAGAGCCTGAAAGG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 AIGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGGTCTGAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-----GAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGA
                                                                                                                      200 ACGIGCGGCCAGAGCIGGGGAAAIGGGCCCGCGAGCCAGGCCGGGCGCTICICCICCIGAI
                                                                                                                                                                                                                                                                                                                                   CTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 GGACGACCAGCTGTTGTGTCCTACAATCACGAGAGTCGCCCTGCAGAGCCTCGCGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 GIGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        596 AATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGCAGGACCA
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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230846 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF080089
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Plate: 48 row: E column: 9
Seq primer: ATTTAGGTGACACTATAG.
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PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
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Sus scrofa
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BF080089
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Design and use of two pooled tissue normalized cDNA libraries for Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="bus_occord"
/db_xref="taxon:g823"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/lab_host="D
                                                                                                                                                        324 ACCAGCTG-TCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGG 266
                                                                                                                                                                                                                                                              565 CCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAAAAACAGTACCGAGGGCT 624
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                  445 TTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364041 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BI339179
BI339179.1 GI:15032462
EST.
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Pred. No. 5.8e-68;
0; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKWARD: GTTTTCCCAGTCACGACG
Plate: 100 row: C column: 24
Seq primer: ATTTAGGTGACACTATAG.
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74.1%;
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Best Local Similarity 74.1
Matches 413; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             685 GGAGAGCAGC 694
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Sus
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

RESULT BI339179 LOCUS

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EST 18-OCT-2000

Euteleostomi; Sus.

BASE COUNT ORIGIN

FEATURES

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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="ul-w.CG0p-bik-0-03-0-UI"
/clone="lib="NLH BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT773D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: The polylinker; Site_1: Not I; Site_2: Eco RI: The NIH BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web Site at brainest.eng.ulowa.edu.
TAG_SEQ=None found"
                                                                   Far: 301 443 1706
Fax: 301 443 1706
Email: mEST@mail.nih.gov
Diligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized considered under appropriate and limited collaborative arrangements following repetitive elements were found in this cDNA sequence: 1-31, >(CAG)n#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 ATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACCATCA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 TGGGCAACTATAACCACAGTAAGGTCACGAAGTTGGGAGTGGTGTCCGAGTCCCACATCC 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 GGCCGGCGCTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTGCAGGGGCGCTTGCTGC
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              onal Institute of Mental Health
Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
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Pred. No. 4.4e-61;
0; Mismatches 106; Indels
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357; Conservative
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20892-9643, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 489)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                /dbxref="txxxn:9923"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="UH10B"
/note="Vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
a 175 c 152 g 93 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AGCGGCCGAAAAGCACCTGGAAGCGCGGTCCGAGCC--GGGAAATGGGCCCACAAAGCCCG 119
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                                                                                                                                                                                                                                                                      Score 276.6; DB 10;
Pred. No. 7.4e-66;
0; Mismatches 109; I
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                                      /organism="Sus scrofa"
    .ocation/Qualifiers
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al Similarity 74.2%;
388; Conservative
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Fax: 301 443 1706

Fax: 301 443 1706

Email: mEST@mail.inh.gov
Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA Clones will be made available by the means for distribution of the BMAP cDNA clones, This fetch will be updated accordingly when that means is determined. The following repetitive elements were found in this CDNA sequence: 3-30. >(CAG)n#Simple_repeat
BODYA=NO.
                                                                               ALSOULU 457 bp mRNA linear EST 15-JUL-1999 UL-M-BGO-aib-g-10-0-UI.S1 NIH_BMAP_MSC Mus musculus cDNA clone AL850020
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
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TAG_TISSUE=spinal-cord
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694 CAGAACC 700
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DEMYSLIZ 455 bp MRNA linear EST 05-0CT-2000 UI-M-CG0p-bil-h-10-0-UI.SI NIH_BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CG0p-bil-h-10-0-UI 3', mRNA sequence.
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
considered under appropriate and limited collaborative arrangements
The following repetitive elements were found in this cDNA sequence:
1-31, >(CAG)n#Simple_repeat
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                 800
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/lab host="DH10B (life Technologies)"
/note="Vector: pr713D-pac (Pharmacia) with a modified
polylinker; site_l: Not I; Site_2: Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
621 GGCTACTGGAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACTG 680
                                                                                                                                                                                                                                                                                                                                                   801 TIGCIGGAGCIGGGAGAGGIGITITGGACCAACAAGIGCCICCITIGGIGAAGGIGACA 860
                                                                                                                                                                                                                                                                                                                                                                                     325 CTCCTGGAGCTGGGGAGAGGCGTTCTGGGACAGCAAGTGCCTACTTTGGTGAAAGTGACT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 GATTGGAGGAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAG
                                                                                                                                                 741 ATTCGGGCCAGGCAAAAAAGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGAG
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0p-bil-h-10-0-UI"
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    .455
    /organism="Mus musculus"

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TEL: 301 443 1706
Fax: 301 443 9890
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KEYWORDS
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 06-FEB-1997
ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.ulowa.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA217236

464 bp mRNA linear EST 06-FEB-15
mu89b05.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
IMAGE:652689 5' sinilar to TR:0340354 G940354 CLASS I
HISTOCOMPATIBILLITY ANTIGEN-LIKE PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:398537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              920
                                                                                                                                                                                                                                                                                                                                                                                                     740
                                                                                                                                                                                                                                                                                                                                                                                                                        206 AACTGGAGCGCAGCCAGGCCAGGGCCACCAAGGTGGAATGGGACGAGCACAAG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 ATCCGTGCCCAAACAGAACAGGGACTACCTGGAGAAGGACTGCCCCGAGCAGCTGAAACGG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385
                                                                                                                                                                                                                                                                      680
                                                                                                                                                                                                                                                                                                                                                  116 GGCTTCTGGAGATATGGTTATGACGGGCAAGATCACCTGGAATTCTGCCCCCAAGACACTA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      801 TIGCIGGAGCIGGGGAGAGGIGTITIGGACCAACAAGIGCCICCITIGGIGAAGGIGACA 860
                                                                                                                                                                                                                                                  561 GAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAG 620
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                             GGCTACTGGAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             741 ATTCGGGCCAGGCAGAACAGGGCCTACCTGGAGAGGGACTGCCCTGCAGAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 CTCCTGGAGCTGGGGAGAGGCGTTCTGGGACAGCAAGTGCCTACTTTGGTGAAAGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                861 CATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATTGGAGAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra MyMouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
                                                                                                                                                                        17.2%; Score 248.4; DB 10; Length 455; 79.5%; Pred. No. 4.9e-58; Live 0; Mismatches 76; Indels 0;
                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA217236.1 GI:1826237
                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACATCACTA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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AA217236/c
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Matches
                                                                                                 BASE COUNT
ORIGIN
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JOURNAL
COMMENT
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KEYWORDS
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3'j; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p1713 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W21141 268 bp mRNA linear EST 20-AUG-1996 zb51g06.rl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307162 5', mRNA sequence.
                                                                                                                                                                                                                                                                                           /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                      569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 ATCATGGGCAACTATAACCACAGTAAGGTCACGAAGTTGGGAGTGGTGTCCGAGTCCCAC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                630 AAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAGA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 AGATATGGTTATGACGGGCAAGATCACCTGGAATTCTGCCCCAAGACACTAAACTGGAG-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474 CTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534 ATTATGGAAAATCACAACCACAGCAAG---------GAGTCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIGCGTTCACACTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 AGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 464;
  on wrong strand
                                                                                                       /strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:652689"
/clone_lib="Soares mouse lymph node NbMLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 231.6; DB 9;
Pred. No. 2.4e-53;
0; Mismatches 89;
                       Seq primer: -28m13 rev2 ET from Amersham
Location/Qualifiers
reversed clone: similarity
                                                                                                                                                                                                                           /tissue_type="lymph node"
/dev_stage="4 weeks"
                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          690 GCAGCAGAACCCAGGGCCTGGCCC 713
                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 GCAGCCGAGCCAGGCCTGGGCAC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%;
74.3%;
                                                                                                                                                                                                      /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:1298018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 330; Conservative
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Exa: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRImers
                                                                                                                                             Bos taurus
Bukaryotas Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

I (bases I to 546)
Smith, T.P. L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
Pertan, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertan, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            561 GAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAG 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             741 ATTCGGCCCAGGCAGACAGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGGGG 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 546;
         214520 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BE809138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 214.6; DB 1
Pred. No. 1.4e-48;
0; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                801 TTGCTGGAGCTGGGGAGGTGTTTTGGACCAACAAG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 71 row: A column: 5
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                  GI:10240250
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85.9%;
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Best Local Similarity
                                                                  BE809138.1
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MEDLINE
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VERSION
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/clone_lib="Soares_fetal_lung_NbHL19w"
/dev_stage="I-9 weeks"
/dev_stage="I-9 weeks"
/lab_host="D410 weeks"
/lab_hos
                                                                              Hiller, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, R., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, R., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Generation and analysis of 280,000 human expressed sequence tags
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1642 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 173.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1201 TAATATTAAGGAAGAGGCAGGGTTCAAGAGGAGCCATGGGGCCACTACGTCTTAGCTGAAC 1260
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                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 226.4; DB 10; Length 268; Pred. No. 5.1e-52; 0; Mismatches 1; Indels 1;
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Best Local Similarity 99.2
Matches 238; Conservative
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Fax: 314 286 1810
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                                                                                                                  AUTHORS
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B1452668 831 bp mRNA linear EST 21-AUG-2001 603169877F1 NCI_CGAP_Mam5 Mus musculus CDNA clone IMAGE:5249395 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapba-rémail.nih.gov
Tissue procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Http://mage.llnl.gov
Plate: LLAM11629 row: j column: 20
High quality sequence stop: 818.
                                                                                                                                                                                                                                                                                                                   354 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 413
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
174 CCAAAAGAAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGAAATGGGCCCGCGA 233
                                                    69 AGTGAAGACCGGTGGACCCAGC----TGAGGACATGAGCCTATCAGCTGGGCTCCCT 121
                                                                                                                                                                                                                                                                                                                                                  302 AGTCGCCGTGCTGAGCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGG
                                                                                                            GCCAGGCCGGCGCTTCTCCTCCTGTGATGCTTTTGCAGACCGCGGTCCTGCAGGGGCGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                          414 AGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG
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                           481 bp mRNA linear EST 26-NOV-2001 CDNA clone G370002P09 5', mRNA sequence. BB851691 G1:17093145
                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases I to 481).

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Tto, M., Kawai, J., Kolima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Saski, D., Sato, K., Shinata, K., Shinaki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akhira, S., Tanaka, T., Tomaru, H., Tagawa, Watahiki, A., Yasanishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-reseggs.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Mayatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNa libraries for rappid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
i.S., Kawai,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Sciences Cencer(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-7.2 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
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134 c 112 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 TCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCCGTTTCCCCGCCCC 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \Upsilon. and Hayashizaki, \Upsilon. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.7%; Score 211.2; DB 9; Length 481; 68.8%; Pred. No. 1.1e-47;
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0; Mismatches 133;
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URL:http://genome_gsc.riken.go.jp,
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Hayashizaki,Y.
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0; Mismatches 137;
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Bukaryota; Metazoa; Chordata; Sclurognathi; Muridae; Murinae; Mus.
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Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishli,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
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Saito,R., Sakai,C., Sakai,K., Sakazume,N., Saski,D., Sato,K.,
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RIKEN Encyclopedia of Mouse Full-length cDNAS (Akimura,T., et al.
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BB858165 GI:17099619
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmid-based cDNA library following identification of the HH locus in the HLA region of chromosome 6. A single mutation (24d1) in the HH gene a ppears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. It results in a critical disulphide bridge important for secondary structure. The cillowing are claimed: a 10825 bp genomic DNA sequence (I) (see AAT96690), the HH 437 bp cDNA sequence (Ia) and their 24d1, 24d2 and contraines; a cloning or expression vector; host cells; a peptide product chosen from the HH gene product, its variants (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method contest, and all inferentiation factors and therapeutic agents for mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigates oligonucleotide directed against a transcriptional product of a nucleic acid sequence as above; and oligonucleotides covering a range of nucleotides from the HH pene. The invention also relates to methods for screening of the HH homozyotes, to HH disease, including gene therapy, the protein and antibody-based therapeutics, and entided gene therapy, and small molecule
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                                                                                                                                                                                                                                                                                   HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss
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This sequence represents the haemochromatosis (HC) gene. Mutations in this sequence are detected using the method of the invention. The method is for identifying an individual with heredizary haemochromatosis (HH) or parelisposition to develop HH or to genetically pass on HH to an offspring, comprising isolating a biological sample and amplifying a region of genomic DNA in the biological sample encompassing all or part of the DNA between markers D6S265 and D6S276, and detecting at least one homozygous or heterozygous mutation in a nucleotide within the region. The method can also be used for identifying an individual with an genetically pass on an ARD to an offspring, comprises isolating a biological sample from the individual and screening genomic DNA in the sample for the presence of a homozygous or heterozygous mutation in a gene, the normal function of which, is required to prevent progression of the disorder. The method(s) can be used to identify individuals that are homozygous or heterozygous (carriers) for the mutation causing the ARD. Especially the method is used to diagnose HH or predisposition to HH by detecting a Cys/82Tyr substitution. Individuals homozygous for this
1380
                                                                                                                                                                                                                                                                                                                                                                                                  gene; HH identification; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of autosomal recessive disorder – particularly hereditary haemochromatosis, by detecting a mutation in the HC gene
                                                            1321 AGGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGGAGTTGAACCTAAACATAGAAAT
                                                                                                                                                                     1381 TGCCTGACGAACTCCTTGATTTTAGCCTTCTGTTCATTTCCTCAAAAAGATTTCCCCA
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Sequence, 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 other;

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 human hemochromatosis
                                                              Length 1440;
                           other
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a defective
                                                              99.9%; Score 1438.4; 99.9%; Pred. No. 0;
                                                                           Pred. No. 0;
0; Mismatches
                         G; 331
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 individuals having
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Matches 1439; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to hereditary hemochromatosis gene products, These proteins may be used to treat a patient diagnosed as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wolff
                                                                CAGGCCTGGATCAGCCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCA
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        1021 ggataaccttggctgtacccctggggaagagcagagatatacgtaccaggtggagcacc
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16-APR-1996;
23-MAY-1996;
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having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacemen therapy for individuals having a defective human hemochromatosis gene.
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Pred. No. 0;
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Best Local Similarity 99.9%;
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GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Human hereditary hemochromatosis 24d1/2 mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss
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iron overload. They may also be used in protein replacement individuals having a defective human hemochromatosis gene.
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              products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for
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        to hereditary
                                                                                                            Score 1436.8;
Pred. No. 0;
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                                                                              Sequence 1440 BP; 348 A; 354 C; 407
        relates
                                                                                                            Query Match 99.8%;
Best Local Similarity 99.9%;
Matches 1438; Conservative
         invention
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                                                            therapy for
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                                               CAGGCCTGGATCAGCCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCA 1140
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                                                                                                                      TIGGAGICATCAGIGGAATIGCIGITITIGICGICATCTIGITCATIGGAAITITGIICA 1200
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                                                                                                                                                                                                                                                                                                                     CDNA sequence encoding a histocompatibility iron loading (HFE) protein.
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ctcctttggtgaaggtgacacatcatgtgacctcttcagtgaccactctacggtgtcggg
             CCTTGAACTACCCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGG
                                       961 ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCT
                                                                 GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACC
                                                                                                   TGCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAGATTTCCCCA
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S65C"
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G93R"
                                                                                                                                                                                                                                                                                                                                 Human; histocompatibility iron loading protein; HFE protein; major histocompatibility complex; non-classical class I gene; chromosome 6p; iron disorder; haemochromatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 "if this base is mutated to G, then protein contains the mutation H63D"
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"if this base is mutated to C,
protein contains the mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
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"if this base is mutated to C, then the
protein contains the mutation 1105T, which
is associated with an Iron overload disorder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 ATGGGCCCGCGAGCCAGGCCGGCGTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTG
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Pred. No. 0;
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100.0%; Pre/
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314
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P-PSDB; AAB19149.
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14-SEP-2000;
14-SEP-2000;
Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
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                                                                                                   GITITIGGACCAACAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTG
                                                                                                                            ACCACTCTACGGTGTGGGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTG
                           AGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGG
                                                                         GCCTACCTGGAGAGGGACTGCCTGCACAGCTGCAGCAGTTGCTGGAGGTGGGGGAGGGT
GATGGGCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCC
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The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM434497-AAM43660) useful for preventing, treating cor ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, or breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, cutofinmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, connis disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis, (c) cardiovascular disorders such as mycardial ischaemias; od) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections. But was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                             Ruben SM;
                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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P-PSDB; AAM43591.
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WPI: 1997-512743/47.
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             "G to A substitution (24d1 mutation associated with HH), results in Cys to
                                                                                                                                                                                                                                                                                      mutation)
                                                                                                                                                                                                                                                                                                             A to T substitution (24d7 variant) results in Ser to Cys substitution"
                                                                                                                                                                                                                                                                                      C to G substitution (24d2 mutation) results in His to Asp substitution
                                                                                                                         haemochromatosis; metal toxicity; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomas WJ;
                                     CCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                        Drayna DT, Feder JN, Gnirke A, Ruddy D,
Isuchihashi Z, Wolff RK;
                                                                                                                              gene therapy; prenatal screening; human; ds
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96US-0632673.
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16-APR-1996;
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This genomic DNA sequence corresponds to the human gene whose mutated form is associated with hereditary haemochromatosis (HH).

To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HIA region of chromosome 6. A physical clone coverage was then generated cterending from D6265, which is a marker that is centromeric of HLA-A, in a telomeric direction through D6276, a marker at which the allelic association was no longer observed. A single mutation the allelic association was no longer observed. A single mutation of isease. This comprises a G to A substitution that is present in G84 of affected chromosomes and in 4% of unaffected chromosomes. Tr results in a cys tor yr substitution in the encoded protein (see AAW36699) at a critical disulphide bridge important for secondary structure. The following are claimed: the HH genomic DNA (I), a structure. The following are claimed: the HH genomic DNA (I), a structure. The following or expression vector; host cells; a cloning or expression vector; host cells; a condition of the main and 24d7, or a peptide of the common HH gene to determine the presence or absence of the common HH gene to determine the presence or absence of the common HH gene contigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mappentic agents for activity in connection with HH disease, an antisode of sequence as above; and oligonucleotides from the armserilation and oligonucleotide directed against a transcriptional corporation and sequence as above; and oligonucleotides from the HH gene. The HH gene to method for detecting a polymorphism in the HH decompleted of a nucleic acid sequence as above; and onligonate of the HH gene. The HH gene to method for or pairs of oligonucleotide directed against a 
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Hereditary haemochromatosis gene and variants – useful for diagnosis and treatment of hereditary haemochromatosis disease
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                                                                                                                                      Disclosure; Fig 3; 115pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                      or polypeptides, useful patient, and as a metal
                                                         ggagcagggaagggaaggaatttgcttcctgagatcatttggtccttggggatggtgg
                                                                                     AGCAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAGAAAGGCACAAAGATTCGGGC
                                                                                                                                              CAGGCAGAACAGGGCCTACCTGGAGGGACTGCCCTGCACAGCTGCAGCTTGCTGGA
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                                                                                                                                                                                                                                                                                 hereditary hemochromatosis; chelation agent; ell differentiation factor; iron overload; ds
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P-PSDB; AAB36869.
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iron overload. They may also be used in protein replacemer individuals having a defective human hemochromatosis gene.
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                                                                                                            Score 321; DB 22; 1
Pred. No. 8.6e-82;
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alleviating iron overload. They may also be
therapy for individuals having a defective h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAAAATCACAACCACAGCAAG-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGGGGAGAGGTGTTTTGGACCAACAAG
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                                                                                                               22.3%;
11 Similarity 72.1%;
540; Conservative
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                                                                                                                 Query Match
                  therapy
                                                                                                                                 Best Local
Matches 54
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4361
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    4182 aaatagggacctattcctttggttgcagttaacaaggctggggatttttccagagtccca 4241
                                                                                                                                                                                              748
                                            CACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTG
                                                                                    GAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAG
                                                                                                 AGCAGCAGAACCCCAGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAAGATTCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; histocompatibility iron loading protein; HFE protein, major histocompatibility complex; non-classical class I gene; chromosome 6p; iron disorder; haemochromatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA of a histocompatibility iron loading (HFE) gene.
                                                                                                                                                                                                                                                                 GCTGGGGAGAGGTGTTTTGGACCAACAAG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1028..1324
                                                                                                                                                                                                                                                                                                                                                  AAA96794 standard; cDNA; 12146
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4652..4915
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5125..5400
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/*tag= f
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6494..6769
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1325..4651
/*tag= b
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/*tag= d
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6928..7041
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/number= 3
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/number= 5
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                                                                                                                                                                                                                                                                                                                                                                                                                 products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4062 cagagetttteatetttteatgeatettgaaggaaacagetggaagtetgaggtettgtg 4121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4122 ggagcagggaagagggaaggaatttgcttcctgagatcatttggtccttggggatggtgg 4181
                                                                                                                                                                                                                                      Tsuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tggaaaatcacaaccacagcaagggtatgtggagagggggcctcaccttcctgaggttgt 4061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGAGAGTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                    New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --GAGTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to hereditary hemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAAAATCACAACCACAGCAAG---------
HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 321; DB 22;
Pred. No. 8.6e-82;
0; Mismatches 0;
                                                                                                                                                                                                                                      Ruddy D,
                                                                                                                                                                                                                                      Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 3; 108pp; English.
                                                                                                                                                  96US-0630912.
96US-0632673.
96US-0652265.
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72.1%;
                                                                                                                          97US-0834497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 540; Conservative
                                                                                                                                                                                                           (BIRA ) BIO-RAD LAB INC
                                                                                                                                                                                                                                     Drayna DT,
                                                                                                                                                                                                                                                                           WPI; 2001-006341/01.
P-PSDB; AAB36870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                           Homo sapiens
                                                                                                                         04-APR-1997;
                                                                                                                                                                  16-APR-1996;
23-MAY-1996;
                                                                   US6140305-A
                                                                                               31-OCT-2000
                                                                                                                                                    04-APR-1996
                                                                                                                                                                                                                                      Thomas WJ,
                                                                                                                                                                                                                                                  Feder JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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5012 ggagcagggaagagggaaggaatttgcttcctgagatcatttggtccttggggatggtgg 5071
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                                                                                                                                                                                                688
                                                                                                                                                                                                                                                                               748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis (HH) affected individual. Also described is a method to determine the presence of absence of the common hereditary haemochromatosis (HFE) gene mutation in an individual comprising: (a) providing DNA or RNA from the individual; and (b) assessing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hereditary haemochromatosis subregion from an HH affected individual
                                                                                                                                       689 AGCAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGC
                                                                                                                                                                                                                                                                                                      5312 caggcagaacagggcctacctggagagggactgcctgcacagctgcagcagttgctgga
                                                                             5072 aaatagggacctattcctttggttgcagttaacaaggctggggatttttccagagtccca
                                                                                                                                                                                                  GAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAG
                                                                                                                                                                                                                                                                                                                                                               749 CAGGCAGAACAGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGTTGCTGGA
                                                                                                                     CACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                    Thomas WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 9; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV57903 standard; DNA; 237326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US17658
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96US-0724394
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Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROG-) PROGENTIOR INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09814466-A1
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01-0CT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the human histocompatibility iron loading (HFE) gene. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene lad to iron disorders. The specification describes a method for disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number 160319). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder
                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgittgaagctitgggctacgiggatgaccagcigticgigtictaigatcatgagagic 4771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4952 cagagetttteatetttteatgeatettgaaggaaacagetggaagtetgaggtettgtg 5011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. haemochromatosis, or a genetic susceptibility to develop it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels 209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 321; DB 21;
Pred. No. 9.1e-82;
                                                                                                                                                                                                                                                                                                                         Barton JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 21-28; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         538 TGGAAAATCACAACCACAGCAAG-----
                                                                                                                                                                                                                                                                                                                       Sawada-Hirai R,
                                                                                                                                                                                                                                                                             (BILL-) BILLUPS-ROTHENBERG INC
                    /*tag= 1
/number= 6
10206..10637
/*tag= m
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72.1%;
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9051..10205
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                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-647244/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                       BE,
                                                                                                                   WO200058515-A1
                                                                                                                                                                                                                                          26-MAR-1999;
                                                                                                                                                          05-OCT-2000
                                                                                                                                                                                                                                                                                                                       Rothenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
  intron
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DNA or RNA for the presence or absence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BFF genes, which are homologues of the milk protein butyrophilm (BF), and can be used in the production of agonists and antagonists of BF function. Also described are: (1) a RORET gene which can be used to develop products for the study, diagnosis and treatment of luupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can similarly be used for hypophosphatemia.
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                                                                                                                                                                                                                                               Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;
                                                                                                                                                                                                                                                                                               Length 237326;
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                                                                                                                                                                                                                                                                                               Score 321; DB 19; Pred. No. 3.9e-81; 0; Mismatches 0;
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Best Local Similarity 72.1%;
Matches 540; Conservative
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                                                                                                                               HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds.
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                                                                                                   Human hereditary hemochromatosis
            BP
            AAC68427 standard; DNA; 10825
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96US-0632673.
96US-0652265.
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16-APR-1996;
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                                                                                                             Length 10825;
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                                                                        Sequence 10825 BP; 2999 A; 2252 C; 2648 G; 2926 T; 0 other;
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Pred. No. 2.5e-81;
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Sequence 7, A Sequence 5, A Sequence 3, A Sequence 20, Sequence 20, Sequence 20,

Sequence

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Sequence 13, Sequence 21, Sequence 21, Sequence 21, Sequence 5, A Sequence 5, A Sequence 9, A Sequence 9, A

Sequence 21, Appl Sequence 5, Appl1 Sequence 10, Appl Sequence 7, Appl1 Sequence 7, Appl1 Sequence 37, Appl1 Sequence 4, Appl1

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APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94111-3834

ZIP: 94111-3834

COMPUTER READBLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265

FILING DATE: 23-MAY 1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
               US-09-503-444A-7
US-08-612-124-5
US-08-652-2673-3
US-08-652-265-20
US-08-632-444A-20
US-08-632-6738-4
US-08-632-6738-4
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US-08-834-497A-21
US-08-890-719-5
US-08-890-719-9
US-08-890-719-7
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1795:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-652-265-9; Sequence 9, Application US/08652265; Patent No. 6025130; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replace(408, "c")
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TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: replace
NAME/KEY: CDS
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4472.841 Million cell updates/sec
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Sequence 11,
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Sequence 12
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                                                                                                                              June 19, 2002, 06:38:35; Search time 79.08 Seconds
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}
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-834-497A-9

US-08-652-265-11

US-08-652-265-11

US-08-834-497A-11

US-08-834-497A-11

US-08-834-447A-11

US-09-503-444A-11

US-08-834-497A-12

US-09-277-457-1

US-08-834-497A-1

US-08-834-497A-1

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US-09-503-444A-1

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US-09-503-444A-1

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S-08-724-394A-21
S-08-724-394A-22
S-08-652-265-5
S-08-652-265-7
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Sequence 9, Application US/08834497A

Patent No. 6140305:
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Taudhinashi, Zenta
APPLICANT: Tsudhinashi, Zenta
APPLICANT: Tsudhinashi, Zenta
APPLICANT: Tsudhinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHRON, NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREFT: 1155 Avenue of the Americas
CITY: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2811
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                   NAME/KEY: allele
LOCATION: replace(1066, "g")
COTHER INFORMATION: /phenotype= "normal
COTHER INFORMATION: (unaffected)"
US-08-652-265-9
                                                                         "normal
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OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d2
FEATURE:
NAME/KEY: allele
LOCATION: replace(414, "a")
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d7
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Best Local Similarity 100.
Matches 1440; Conservative
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          541 AAAATCACAACCACGAAGGAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGC
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(unaffected)"
/label= 24d7
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(unaffected)"
/label= 24d1
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                                                                                                                                                                                       NAME: Poissant, Brian M.
REGISTRATION NUBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFRAX: 650-493-5556
                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
                                                                                                 FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
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/label= 24d2
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OTHER INFORMATION: 'Checkprotype
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OTHER INFORMATION: /label= 24
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
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LOCATION: replace(414,
OTHER INFORMATION: /phe
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TOPOLOGY: linear
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LOCATION: 222..1268
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LOCATION: replace
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              CLASSIFICATION:
 FILING DATE:
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Matches 1440;
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                     TGCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCCA
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/label= 24d2
                                                                                                                                                                                                                                                                   APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gulrke, Andreas
APPLICANT: Gulrke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING LAST: 14-Feb-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/65,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTONNEY/AGENT INFORMATION:
NAME: POISSART, BITAN N.
RECISTRATION NUMBER: 28,462
RECISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                               Sequence 9, Application US/09503444A Patent No. 6228594 GENERAL INFORMATION:
                                                                                                                                                                                                                                                APPLICANT: Thomas, Winston J. APPLICANT: Drayna, Dennis T
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TELEX: 66141
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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OTHER INFORMATION:
FEATURE:
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NAME/KEY: allele
LOCATION: replace
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STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                Length 1440;
                                                                                                                                                                                                                         0; Indels
            /phenotýpe= "normal or wild-type (unaffected)" /label= 24d7
                                                                                                          wild-type
                                                                                                                                                                                               DB 4;
LOCATION: replace(414, "a")

COTHER INFORMATION: (phenotype="normal or OTHER INFORMATION: (unaffected)"

COTHER INFORMATION: (label=24d7)

FEATURE:

NAME/KRY: allele

LOCATION: replace(1066, "g")

COTHER INFORMATION: (phenotype="normal or OTHER INFORMATION: (unaffected)"

COTHER INFORMATION: (label=24d1)

US-09-503-444A-9
                                                                                                            or
                                                                                                                                                                                            100.0%; Score 1440;
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 1440; Conservative
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FEATURE:
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                                                       CCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGG 960
             CTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGG
                                                                                                                                                                                                                                                                                                   APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08652265 Patent No. 6025130 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
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ADDRESSEE: Townsend
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                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: replace(1066, "a")
COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
COTHER INFORMATION: /label= 24dl
US-08-652-265-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1438.4;
Pred. No. 0;
0; Mismatches
NAME: Smith, William M.
REGISTRATION NUMBER: 30.223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.98;
99.98;
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Best Local Similarity 99.9
Matches 1439; Conservative
                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 222..1268
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MOLECULE TYPE: cDNA
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US-08-652-265-11
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AATTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGGGCCTGGCCCACCAAGC 720
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                         AATTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGGGCCTGGCCCACCAAGC
                                                        TGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTACCTGGAGAGGGACT
                                                                       GCCCTGCACAGCTGCAGCTGCTGGAGCTGGGGGAGGGTGTTTTGGACCAACAAGTGC
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Rolirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary He
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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Patent No. 6025130
GENERAL INFORMATION:
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STATE: California
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   COMPUTER KEDABLE FORD.

MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPAILSE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 17957-000500
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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99.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.9
Matches 1439; Conservative
                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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222..1268
COMPUTER READABLE FORM:
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LOCATION: replace
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LOCATION:
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APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TTLE OF INVENTION: HERBITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: New York
STREET: New York
CITY: New York
COUNTRY: USA
ZIP: 10036-2811
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis;
OTHER INFORMATION: /label= 24d1
US-08-834-497A-10
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                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows 95
SOFTWARE: FastSEQ for Windows 95
SOFTWARE: FastSEQ for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.9%; Score 1438.4; 99.9%; Pred. No. 0;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 99.9
Matches 1439; Conservative
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222..1268
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LOCATION:
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                                                               541 AAAATCACAACCACAGGAAGGAGTCCCACACCCTGCAGGTCATCCTGGGGCTGTGAAATGC
                                                                                                                                                                                                                               AATTCTGCCCTGACACACTGGATTGGAGGAGCAGCAGAACCCAGGGCCTGGCCCACCAAGC
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Db 1201 TAATATTAAGGAAGAGGCAGGGTTCAAG Qy 1261 GTGAGTGACACGCAGCCTGCAGACTCACAGACTCACAGAGCAGCAGCAGCAGACTCACAGAGCAGCAGCAGCAGACGCAGCAGCAGCAGCAGCATTATGAGACTCATGAGAGAGA	RESULT 7 US-08-834-497A-11 ; Sequence 11, Application US/0883449; ; Patent No. 6140305 ; GENERAL INFORMATION: ; APPLICANT: Thomas, Winston J. APPLICANT: Drayna, Dennis T.	2883	STREET: 1155 Avenue of the Amm: CITY: New York STATE: New York COUNTRY: USA 2.TP: 10036-2811 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	COMPUTE: LBM PC COMPUTINE COMPUTE: LBM PC COMPUTINE SOFTWARE: FastSEG for Windows CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/834 FILING DATE: 04-APR-1997 CLASSIFICATION BTA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: CLASSIFICATION DATA: COMPUTE: 04-APR-1997 CLASSIFICATION DATA: 05-APR-1997	US OB (-1996 1 US OB (-1996 1 US OB	APPLICATION NUMBER: US 08/630, FILING DATE: 04-APR-1996 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: POISSANT, Brian M. REGISTRATION NUMBER: 28,462 REFERENCE/DOCKET NUMBER: 8907. TELECOMMUNICATION INFORMATION:	TELEPHONE: 650-493-4935 TELEFAX: 650-493-5556 TELEX: 66141 PENNIE SOUGHCE CHARACTERISTICS: LENGTH: 1440 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
	361 TTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCTATGATCATGAGAGTCGCC 420	TGAGTCAGAGTCTG	601 AAGAAGACAACGAGGGCTACTGGAAGTACGGGTATGGAGGACCACCTTG 660 111111111111111111111111111111111111	721 TGGAGTGGGAAAGGCACAAGATTCGGGCAGGACAACAGGGCCTACCTGGAGAGGGACT 780	### 1 CTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGG 900	961 ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGATGGGACCTACCAGGGCT 1020	1081 CAGGCCTGGATCAGCCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCA 1140
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ACTGTGGGAAGGACAAAACTAGAGACTCAAAG 1320
                                          AGAGGAGCCATGGGGCACTACGTCTTAGCTGAAC 1260
                                                                      HEMOCHROMATOSIS GENE PRODUCTS
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Americas
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CAGGCCTGGATCAGCCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCA 1140
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  841 CTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGG 900
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                            CCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGTGAATGG
                                        GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/09/503,444A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows 95
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FILING DATE: 14-Feb-2000
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York STATE: New York
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                                                                                                                                                                                                                                                                                                                 CCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCCGTTTCCCCGCCCCCCAAAAG 180
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                                                                                                                                                    Length 1440;
                        , LOCATION: replace(408, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
; OTHER INFORMATION:
; OTHER INFORMATION: /label= 24d2
US-08-834-497A-11
                                                                                                                                                                             1; Indels
                                                                                                                                                   DB 3;
                                                                                                                                                Score 1438.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                99.98;
                                                                                                                                                             Best Local Similarity 99.9
Matches 1439; Conservative
                       FEATURE:
NAME/KEY: allele
LOCATION: replace(
OTHER INFORMATION:
NAME/KEY:
LOCATION:
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Patent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Grike, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TILE OF INVENTION: Hereditary Hemoc
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US-09-503-444A-11
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 24d1
OTHER INFORMATION: /label= 24d1
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Pred. No. 0;
0; Mismatches
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TELEPHONE: 212-790-9090
TELEPHONE: 212-869-9741
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISSART, BIAIR M.
                                                                                            NAME: Poissant, Brian M. REGISTRATION NUMBER: 28,462
                                                                                                                                                                                                    10:
                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10 SEQUENCE CHARACTERISTICS: LENGTH: 1440 base pairs TYPE: nucleic acid
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Best Local Similarity 99.9%;
Matches 1439; Conservative
                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 222..1268
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LOCATION: replace
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d2
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                                                                                                                                                                                                                                                                                                                                                                                NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                           SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILLIG DATE: 14 Feb-2000
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-may-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPERATING SYSTEM: WordPerfect Version
                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 222..1268
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  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                            STREET: 1155 AV CITY: New YORK STATE: New YORK
                                                                         New York
                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                      USA
                                                                                                10036
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                                                                                      COUNTRY:
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                                        1381 TGCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTGATTTCCTCAAAAGATTTCCCCA
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LOCATION: replace(408, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 2442
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Hereditary Hemochromatosis
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /phenotype= "Hereditary; OTHER INFORMATION: /label= 24d1
US-08-652-265-12
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99.9%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                      Sequence 12, Application US/08652265
Patent No. 6029130
PAPELICANT: Thomas, Winston J. APPLICANT: Thomas, Winston J. APPLICANT: Feder, John N. APPLICANT: Reder, John N. APPLICANT: Ruddy, David APPLICANT: Tsuchihashi, Zenta APPLICANT: Widff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,23
REFRENCE/DOCKET NUMBER: 17957
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDENESS: single
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Best Local Similarity 99.9
Matches 1438; Conservative
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LOCATION: 222..1268
                                                                                                                                                                                                                                                                                                                                                                     California
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LOCATION: replace
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US-08-652-265-12
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CITY: Sa
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NAME/KEY:
LOCATION:
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 TELEFAX:
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                                                                                1321 AGGGAGTGCATTTATGAGCTCTTCATGTTTTCAGGAGAGAGTTGAACCTAAACATAGAAAT 1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows 95
OPERATE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA: WINDOWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAX-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08834497A Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Dayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY F.
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 890
TELECOMMUNICATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
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ADDRESSEE: Pennie &
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STATE: New York
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis Indels 2; DB 3; 99.8%; Score 1436.8; ilarity 99.9%; Pred. No. 0; Conservative 0; Mismatches /label= 24d1 /label= 24d2 "a") LOCATION: replace(1066, OTHER INFORMATION: /phen OTHER INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 1440 base pairs TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: TYPE: nucleic acid STRANDEDNESS: single CDS 222..1268 OTHER INFORMATION: OTHER INFORMATION: FEATURE: MOLECULE TYPE: CDNA linear NAME/KEY: allele Best Local Similarity Matches 1438; Conserv

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601 AAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGGCAGGACCACCTTG 660
                                                      721 TGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTACCTGGAGAGGGACT
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Petent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Windy, David
APPLICANT: Feder, Winston N.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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CITY: No
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CCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCCGTTTCCCCGGCCCCCCAAAAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /phenotype= "Hereditary Hemochromatosis
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     8907-0088
                                                                                                                                  UMBER: US/09/503,444A
14-Feb-2000
                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 33-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY_AGENT INFORMATION:
                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                28,462
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OTHER INFORMATION: /phenotyj
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SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 222..1268
FEATURE:
                                                                                                                                         APPLICATION NUMBER:
FILING DATE: 14-Feb
CLASSIFICATION:
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		0y 1	1321
241	CGGCCCTTCTCTCTCTTTTCCAGACCGCGTCCTCCAGGGGCGCTTGCTGCTT 300 - - - - - - - - - - - -		1321
301	CACACTOTIGOROTIACOTOTITIA CONTROLOGO CONTROL	Qy 1:	1381
301		Db 11:	381
361		RESULT	13
361		Sequence : Sequence	ence
421	. GTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGC 480 	; Patent N ; GENERAL ; APPLICA ; APPLICA	atent N ENERAL APPLICAI
481	TGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGG		APPLICAN TITLE ON FILE REN
541			CURRENT CURRENT NUMBER
541		Ω	SOFTWAR
601	- AAGAAGACAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGGCGCAGGACCACCTTG 660 	TYI TYI ORC	LENGTH TYPE: I ORGANIS
661	AATTCTGCCCTGACACACTGGATTGGACACACAGAACCCAGGGCCTGGCCCACCAAGC	-	NAME/KI LOCATIC OTHER 1
721	TGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTACCTGGAGAGGACT	à	, Ma
781	TGGAGTGGGAGAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTACCTGGAGAGGGACT GCCCTGCACAGAGCTGCAGAATTGCTGGAGTTGGGGAACAGGGGTTGTTGAAAAAAAA	Best	st Loca tches
781		Qy 2	222
841	CICCITIGGIGAAGGIGACACAICAIGIGACCICTICAGIGACCACICIACGGIGG AICHTHILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	8 & &	1 282
1 00	CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ପ୍	61
901	CCTTGAACTACTACCCCAGAACATCACCATGAAGTGGCTGAAGGATAACCAGTGG 960 	ο _γ 3	342
961	ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGGACTACCAGGGCT		121
961	AIGCCAAGGAGTICGAACCIAAAGACGTAITGCCCAATGGGGATGGGACCTACCAGGGCT 1020		402
1021	GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGCACC 1080	Db 1	181
1021	GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGCACC 108		241
1081	CAGGCCTGGATCAGCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCA 1140 		522 (
1141	TTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCGTAATTTGTTCA 120		301
1141			282
1201	TAATATTAAGGAAGAGGCAGGGTTCAAGAGGAGCCATGGGGCACTACGTCTTAGCTGAAC 126	9 40 ;	361 a
1261	CHORACHAR AND CARONICATION AND CONTRACTOR AND CONTR	Db 4	421
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                                                                                                                                                                                                   ANT: Rothenberg, Barry E.

ANT: Sawada-Hirai, Ritsuko
ANT: Barton, James C.
OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
REFERENCE: 10653/002001
TRAPPLICATION NUMBER: US/09/277,457
TPILING DATE: 1999-03-26
OF SEQ ID NOS: 30
OF SEQ ID NOS: 30
OF SEQ ID WIGHOUS VERSION 4.0
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INFORMATION: Missense mutation at nucleotide 314
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100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                          e 1, Application US/09277457
No. 6355425
INFORMATION:
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1219; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         KEY: mutation
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GCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-652-265-1
| Sequence 1. Application US/08652265
| Patent No. 6025130
| GENERAL INFORMATION:
| APPLICANT: Thomas, Winston J. APPLICANT: Feder, John N. APPLICANT: Feder, John N. APPLICANT: Ruddy, David APPLICANT: Tsuchlhashi, Zenta APPLICANT: Wolff, Noger K. TTILE OF INVENTION: Hereditary Hemochromatosis Gene NUMBER OF SEQUENCES: 44
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1422 CCTCAAAAGATTTCCCCA 1440
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: California
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/note= "No. 6025130mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
allele"
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24d2(C)
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis
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NAME/KEY:

LOCATION:

LOCATION:

OTHER INFORMATION:

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OTHER INFORMATION: /note= "start and stop positions of the Information: normal or wild-type (unaffected) of the Information: sequence surrounding variant for OTHER INFORMATION: allele (SEQ ID NO:20)"
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LOCATION: replace(3872, "c")
COTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)
OTHER INFORMATION: /label= 24d2
FEATURE:
FRATURE: allele
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(unaffected)"
/label= 24d1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
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Pred. No. 8.9e-83;
                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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LOCATION: replace(5834, "g")
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: /label= 24
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72.1%;
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FEATURE:
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FEATURE:
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Best Local Similarity
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3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCT 3821
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LOCATION:
LOCATION:
G040..6153, 7107..7147)

COTHER INFORMATION:
OTHER INFORMATION:
COCATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: genomic sequence surrounding variant
OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)"
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genomic sequence surrounding variant
for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                      MEDLUM TIPE: LIDEA VALSA

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/652,265

FILING DATE: 23-MAY-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: SMITCH, William M.
REGISTRATION NUMBER: 17957-000500

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
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OTHER INFORMATION: /phenotype
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                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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FEATURE:
NAME/KEY:
LOCATION: 5507..602
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US-08-652-265-3
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hes 540; Conserv
                                            94111-3834
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LOCATION:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          748
                                                                         4182 AAATAGGGACCTATTCCTTTGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCA 4241
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                                                                                                                                                                                                                                                  GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 477
                                                                                                                                                                                                                                                                                                                                                 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537
                                                                                                                                                   TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 417
                                                  GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357
  Indels 209; Gaps
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APPLICANT: Wolff, Roger K.
TILLE OF INVORTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, Eighth Floor San Francisco
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0
  Mismatches
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Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
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Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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  Conservative
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Search completed: June 19, 2002, 08:40:03 Job time: 7288 sec

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Seguence Sequence

Homo sapien

Title: Perfect score:

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AJ250635 Homo sapi
AF150664 Homo sapi
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AF008587 Rattus no
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AF176534 RATTUS NO
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Unclassified.
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I (bases 1 to 1440)
Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6143035-A 12 31-OCT-2000;
Location/Qualifiers
1. 1440
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AR117796 SAR149466 AR117794 SAR117795 AR149464 AR117793 AR117793 AR149463 UG0319 HOI
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   June 19, 2002, 08:23:48; Search time 3675.59 Seconds (without alignments) 8198.470 Million cell updates/sec
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
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1 (bases 1 to 1440)
Thomas.W.J., Drayna,D.T., Feder,J.N., Gni
Tsuch,hashi,Z. and Wolff,R.K.
Method for determining the presence or al
hemochromatosis gene mutation
Patent: US 622854 A 12 08-MAY-2001,
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421 GTGGGAGCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC	GATGATGAGA GATGATGAGA
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601 AAGAACAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGGGCAGGACCAC 11	CTGGGCT
661 AATTCTGCCCTGACACTGGATTGGAGAGCAGAGACCCAGGGCCTGGCCCACC	CAGGACC
721 TGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGACAGGGCCTACCTGGAGAGG 	GCCTGGCCCAC
	CTACCTGGAGAG
QY 781 GCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTTTTGGACCAACAGG	TTGGACC
QY 841 CTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC	TACGGTGT
QY 901 CCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCAA'	SATAAGCAGO
QY 961 ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG	ACCTAC
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Qy 1141 TTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTGT	CATTGGAATTT
QY 1201 TAATATTAAGGAAGAGGCAGGGTTCAAGAGGAGCCATGGGGCACTACGTCTTAGCTG	TCTTAGCT
QY 1261 GTGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCA 	탕드탕
Qy 1321 AGGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGA 	TAAACA TAAACA

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homas,W.J., Draypa,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 10 31-0CT-2000;
Local Daries 1. 1440
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99.9%; Pred. No. 0;
iive 0; Mismatches
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Sequence 10 from patent US 6140305.
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AR117794.1 GI:14098700
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Matches 1439; Conservative
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Op	721	TGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAGGGCCTACCTGGAGAGGGAC 780	٥y	
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qq	781	GCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGGGGTGTTTTGGACCAACAGTGC 840	δλ	9
oy	841	CICCTITGGIGAAGGIGACACAICAIGIGGACCICITCAGIGACCACICIACGGIGGGG 900	qα	9
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οy	901	CCTTGAACTACTCCCCGGGAACATCACGTGGAGGTGGGTG	qα	12
QQ	901		Qy	18
Qγ	961	ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCT 1020	qa	18
QQ	961		Qy	24
٥y	1021	GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCGAGATATACGTACCAGGGGGGGCACC 1080	QQ	24
qq	1021		δλ	30
٥y	1081	CAGGCCTGGATCAGCCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCA 1140	qa	30
qq	1081		Qy	36
Οy	1141	TTGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTGTTCA 1200	qa	36
QQ	1141	TIGGACTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCGAATTTTGTTCA 1200	Qy	42
οy	1201		qq	42
qq	1201	TAATATTAAGGAAGAGGCAGGGTTCAAGAGGGGCCATGGGGCCACTACGTCTTAGCTGAAC 1260	Qy	48
ογ	1261	GTGAGTGACACGCGCGCGAGACTCACTGTGGGAAGGACAAAACTAGAGACTCAAAG 1320	qa	48
qq	1261	GTGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAG 1320	Qy	54
δλ	1321	AGGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGTTGAACCTAAACATAGAAAT 1380	qa	54
qq	1321	AGGGRGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAAT 1380	QY	9
ογ	1381	TGCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCA 1440	qa	9
qq	1381	TGCCTGACGAACTCCTTGTTTTTAGCCTTCTCTTTTTTCTCCTCAAAAGATTTCCCCA 1440	δλ	99
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Score 1438.4;
Pred. No. 0;
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D. Tsuchihashi,2. and Wolff.R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 11 31-OCT-2000;
Location/Qualifiers
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840 840 900

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1440 bp US 6140305.

Sequence 11 from patent AR117795 AR117795.1 GI:14098701

AR117795

LOCUS DEFINITION

GI:1409870

Unknown. Unclassified.

REFERENCE AUTHORS

. Unknown.

KEYWORDS SOURCE ORGANISM ACCESSION VERSION

1. .1440 /organism="unknown"

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                    GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGCACC
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hered
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Pred. No. 0;
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Patent: US 6228594-A 10 08-MAY-2001;
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US 6228594
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Sequence 10 from patent
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AR149464.1 GI:15114055
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                                CGGCGCTTCTCCTCATGCTTTTGCAGACCGCGGTCCTGCAGGGGCGCTTGCTGCGGTT
                                                                                              CACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGT
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1 (bases 1 to 1440)
Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a herediihemochromatosis gene mutation
Patent: US 6228594-A 11 08-MAY-2001;
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Pred. No. 0;
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        Hereditary hemochromatosis gene pro
Patent: US 6140305-A 9 31-0CT-2000;
Location/Qualifiers
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Tsuchihashi, Z. and Wolff, R.K.
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TLQYILGCEMQBDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEP
RARQNRAYLERDCPAQLQGLLELGRGVLDQQVPLVKYTHHVTS
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QPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFIILRKRQG
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                                                              Thomas, W., Tsuchihashi, Z., Ruddy, D.A., n.F., Domingo, R., Ellis, W.C., Fullan, A., L., Kimmel, B.E., Kronmal, G.S., Lauer, P., Mapa, F., McClelland, E., Meyer, N.C., N., Moore, T., Morkang, E., Prass, C.E., S.W., Schatzman, R.C., Brunke, K.J., S., Bacon, B.R. and Wolff, R.K.
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M. Kimmel, B.E., Kronmal, G.S., Lauer, P.,
pas, F., McClelland, E., Meyer, N.C.,
M., Moore, T., Morkang, E., Perass, C.E.,
M., Schatzman, R.C., Brunke, K.J.,
Bacon, B.R. and Wolff, R.K.
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/translation="MGPRARPALLLLMLLQTAVLQGRLLPLGYVDDQLFVFYDHESRR
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Direct Submission
Submitted (06-SEP-1999) Oliva R., Faculty of Medicine and Clinic
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Hospital, Human Genome Research Group, Casanova 143, 08036, SPAIN
Location/Qualifiers
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VEPRTPWVSSRISSOMMLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCE
MQDBNGTEGTWKYGYDGQDHLEFCPDTLDWRAAEPRAWPTKLEWERKIRAYL
ERDCPAQLQQLLELGRQVLDLDQOVPPLYVTHHVYSSYTTLKORALNYYPQNITMKWLK
DKQPMDAKEFERPKDLANGGTYGGNITLAYPPGEEDRYTCQVEHFGLDQPLIVIWEP
SPSGTLVIGVISGIAVFVVILLFIGILFILLAKRQGSRGAMGHYVLAERR"
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                                                                                                                                                                                     61 CTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCCGTTTCCCCGCCCCCAAAGA 120
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                                                                                                                                                                                                                             242 GGCGCTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTGCAGGGGCGCTTGCTGCGTTC
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                                                                                            Length 1280;
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Pred. No. 0;
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                                                                                                               Matches 1278;
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ORIGIN
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/codon_start=1
/product="hemochromatosis termination variant terE6"
/product="hemochromatosis termination variant terE6"
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/db_xref="GI:11094315"
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SLFEALGYVDDQLFVFYDHESRRVEPFRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear PRI 07-MAY-2001 variant terE6 (HFE) mRNA,
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Catarrhini; Hominidae; Homo.
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                                                      TGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAGA
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David, V. and Mosser, J.
The HFE gene undergoes alternate splicing processes
                                                                                             1082 AGGCCTGGATCAGCCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCAT
                                                                                                                                                    TGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTGTTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Bernard, Rennes 35043, France
Location/Qualifiers
1. 1200
/ Organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                     GCCTGACGAACTCCTTGATTTTAGCCTTC 1410
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Mammalia; Eutheria; Primates;
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AF115265
AF115265.1 GI:11094314
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/gene="HFE"
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AUTHORS
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JOURNAL
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LOCUS
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KEYWORDS
SOURCE
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RAWPFKLEMERHKIRARQNRAYLERDCPAGLQQLLEFGRGYLDQQVPPLVKYTHHVTS
SVATLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYGGWITLAVPPGE
EQRYTCOVEHFGLLDPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFILLRKRQG
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                                                                                                                                                                            61 CGGGGTCCTGCAGGGGGCGTTGCTGCTGCTCACACTCTCTGCACTACCTCTTCATGGGTG
                                                                                                                                                                                                                                                                                                                         TGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGGAGGAGTCCCACA
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                                                                                     Score 1185.8;
Pred. No. 0;
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ilarity 99.8%;
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Best Local Simi
Matches 1187;
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Homo sapiens hemochromatosis splice variant del14E4 (HFE) mRNA, complete cds.
AF079407
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SLFEALGYVDDQLFVEYDHESRRVEPRTPWVSSRISSQMWLQLSQSKGWDIHFTVDF
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WATIMENHINHSKRSHTRARQVARVLERDQQQLGLELGGRGVLDQQVTTLRCRALNYY
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QPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFITIRRRQGSRGAMGHYVLAERE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                     1020
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GGGAGCCCTCACCGTCTGGCACCCTAGTCATTGGAGTCATCAGTGGAATTGCTGTTTTTG
                        TGGGAAGGAGACAAAACTAGAGACTCAAAGAGGGAGTGCATTTATGAGCTCTTCATGTTT
                                                                                                                                                                                                                                                                                                                         1081 TGGGAAGGAGACAAAACTAGAGACTCAAAGAGGGAGTGCATTTATGAGCTCTTCATGTTT
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                                                                                         TCGTCATCTTGTTCATTGGAATTTTGTTCATAATATTAAGGAAGAGGCAGGGTTCAAGAG
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/protein_id="AAC62646.1"
/db_xref="GI:3695107"
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Pred. No. 7.7e-281;
); Mismatches 2;
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Direct Submission
Direct Submission
Submitted (21-JUL-1998) Immunology, Un.
Court Road, Cambridge CB2 10P, UK
Location/Qualifiers
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Mammalla; Eutheria; Primates; Catar I
(bases I to 1045)
Rhodes, D.A. and Trowsdale, J.
Alternate splice variants of the he
Immunogenetics 49 (4), 357-359 (199
99180629
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chrcmosome="6"
/map="6p22.1"
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MAM 22-OCT-2000

Euteleostomi; Ceratotherium

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PLEEALGYVDDELEVYXVHESRRAESRAQWVLGEAHSOLWLOLSSLKGWDHMFIVDF WITMDNHMESRSHLLOKRAAES WITMDNHMESRSHLLOKRAAES RAITTKLEWENKIRAKONTRACQURAELGRGVLDQVPPLVKVTHHVAS AVTILRCQALNYYDQNJTMRRALKBRREMDVKDAESKDVLPSGDGTYGSWEALLYPPGGE EQRYTLCQUEHPGLDQPLTATWBESLSNTLVTGVISGIAVCVIIFFIGILFRILRKRQA
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/protein_id="AAG2301.1"
/db_xref="G1:1094568"
/tb.xref="G1:1094568"
/translation-"MGPRARPALFFLILLRTVAAQGRPPRSHSLRYLFMGASERDHGL
                                                                                                                                      Ceratotherium simum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium
El (bases 1 to 1320)
E (bases 1 to 1320)
E (bases 1 to 1320)
Direct Submission
L Opublished
Direct Submission
L Swest, C.J., Worley, M. and Beutler, E.
E (bases 1 to 1320)
Direct Submission
L Submitted (29-AUG-2000) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
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mRNA, complete
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Pred. No. 1.8e-252;
0; Mismatches 227;
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/db_xref="taxon:9807"
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Ceratotherium simum HFE protein
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Best Local Simi
Matches 1063;
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                                                                                       306 TCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGTTTGAA
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                                                                                                                                                         GAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGT
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   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Dicerorhinus. I (bases 1 to 1320)
West, C.J., Worley, M. and Beutler, E. Rhinoceros HFE Polymorphisms
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                                                                                         Unpublished
2 (bases 1 to 1320)
West, C.J., Worley, M. and Beutler, E.
Direct Submission
Submitted (29-80G-2000) Molecular and Experimental Medicine,
Scripps Research Institute, 10550 North Torrey Pines Road, Le
Jolla, CA 92037, USA
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Pred. No. 1.8e-252;
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2 (bases 1 to 1319)
West,C.J., Worley,M. and Beutler,E.
Direct Submission
Submitted (29-AUG-2000) Molecular and Experimental Medicine,
Scripps Research Institute, 10550 North Torrey Pines Road, La
Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                              1141 CTGCAGACTCCTTGTGGGGAGGACACATAATTGGAGACTCAGAGGGGGGGCTGCAC-TTGTGG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Rhinocerotidae;
1 (bases 1 to 1319)
West, C.J., Worley, M. and Beutler, E.
Rhinoceros HFE Polymorphisms
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 819)

RS NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Ontact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Gapbs refmail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1711 row: d column: 06

High quality sequence stop: 792.
                                                                                                                                                                                                                                                                                                                                                                          BG747345 819 bp mRNA linear EST 15-MAY-2001 602704818F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857941 5',
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ECORI; CDNA made by oligo-dT priming. Directionally
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B1339179 364041 MA
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BE94943 UT-M-GGQ
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ster than or equal to the score of the result being printed,
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Standard, J., Akzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Buldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayateu, M., Hill, D., Hiramoto, K., Hiracka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Koya, S., Kato, H., Kawat, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Nishi, K., Nomura, K., Numazaki, R., Coho, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, Saito, R., Sakai, C., Sakai, C., Sakai, D., Schain, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                            2 (sites)
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shibata,K., Itoh,M., Alzawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Shibata,K., Itoh,M., Alzawa,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiwaji,K., Yoneda,Y., Ishikawa,T., Ozawa,Y., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan (E-mall:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5 GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTVV 3'], CDNA was prepared by using trehalose thermo-activated reverse transcriptase
                                                                                                                                                                                 Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                            Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2310032M04.
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The RIKEN Genome Exploration Research Group Phase II Team and
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                                                                                                                                                                                                                         Carninci,p. and Hayashizaki,y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mammalia; Eutheria;
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the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
201 c 235 g 181 t
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                                                                                                                                                                                                                                                   GACCAGCTGTTCGTGTTCTATGATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGG 443
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/translation="MSISAGIPVRPLILILILWSVAPQALPPRSHSIRYLFWGASEPDLGLPLFEARGYVDDQLFVSYRHESRRAEPRAPMLLEGTSSQLWLHLSQSLKGWDYMFDLGLPLFEARGYVDDQLFVSYRHESRRAEPRAPMLLEGTSSQLWLHLSQSLKGWDYMFDLGFPRGYVDGDGLFVSYRGYVSEGTRACYSEDGLHEBE CPWFTLWWSAABPGGAWTTKVEMDEHKIRARONRDYLEKDCFPEGLKRLLELGRGVLGGQVPTLVKVTRHWASAABPGGARTKVERDFPGONITWRWLCDNGPLDAKDVNPEKVLRNGGGYVGGVTLAVKVTRHWASTGSLRCQALDFFPGONITWRWLCDNGPLDAKDVNPEKVLRNGGETVGGUTLAVROPETRETCQVBHPGLOQPLTASWEPLQSQAMIIGIISGVTVCAIFLVGIGFTLLELTIKRRKASGGTWGGYVLTDCE"
                           And through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5, Georgian Strand Tranda Tranda
subsequently enriched for full-length by cap-trapper. CDNA went bugh one round of normalization to Rot = 5.0 and subtraction to = 25.0. Second strand CDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="tongue"
/clone_lib="RIKBN full-length enriched mouse cDNA library"
/dev_stage="adult"
99. .1178
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Mismatches 359; Indels 48;
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MGD:MGI:1905246"
/db_xref="taxon:10090"
/clone="2110032M04"
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/db_xref="GI:12844463"
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/note="data source:MGD,
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70.18;
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/organism="Homo sapiens"
/db_xref="taxon:966"
/db_xref="taxon:966"
/clone_lib="Er0209"
/dev_stage="Adult"
/note="Organ: lung_tumor; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from Organs Profit (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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1 (bases 1 to 384)

Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-ET0209-151200-003-F07&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence start: 17
High quality sequence store: 384.
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РМ4-БТО209-151200-003-£07 БТ0209 Homo sapiens CDNA, mRNA sequence.
BF883952
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
979 CTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTAC 1038
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                            468 CTAAAGACGTATTGCCCAATGGGATGGGACCTACCAGGGCTGGATAAACTTGGCTGTAC
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                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. II (bases 1 to 570)

NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incytte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM20 row: j column: 04 High quality sequence stop: 566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620 GGGCTACTGGAAGTACGGGTATGATGGGCAGGACCACTTGAATTCTGCCCTGACACTT 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 GGGCTACTGGAAGTACGGGTATGATGAGGGCAGGACCACCTTGAATTCTGCCCTGACACCACT 167
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                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rêmail.nih.gov
Tissue Procurement: DCTD/DTP
   BE272926
BE272926.1 GI:9147279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Email: Smith@email.marc.usda.gov
Email: Smith@email.marc.usda.gov
Single pass Sequencing. Bases called and alt trimmed with phred
v0.980904 e. Vector identified by cross_match with the -minscore 18
PCR PRIMERS
FORRARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCGAGTAGGAC
Flate: 100 row: C column: 24
Seq primer: ATTTAGGTGACATATAG.
                                                                                                                                                                                                                                                                                                                                                                                                             pig.
Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 550)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                  EST 30-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
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                                                                                                                146
324 ACCAGCTG-TCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGG 266
                                  504
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                                                                                      564
                                                                                                                                            624
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                                                                               565 CCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCT
                                            TTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGG
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Pred. No. 9.3e-68;
0; Mismatches 114; Indels
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/db_xref="taxon:9823"
/clone_lib="MARC_2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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74.0%;
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Best Local Similarity 74.0
Matches 412; Conservative
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, B. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. Design and use of two pooled tissue normalized cDNA libraries for Unpublished (2000)
                                                     200 ACGIGCGGCCAGAGCIGGGGAAAIGGGCCCGCGGAGCCAGGCCGGCGCTICTCCTCCTGAI 259
                                                                                                                                                                        380 GGATGACCAGCTGTTCGTGTTCTATGATGAGAGTCGCCGTGTGGAGCCCCGGACTCC 439
                                                                                                                                                                                                                                                                                                                                                                                                           440 AIGGGTITCCAGTAGAAITICAAGCCAGAIGIGGCIGCAGCIGAGGICAGAGICIGAAAGG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                     294 CIGGCICICGGGTAAGGCCICCAACCAACTGTGGCIGCAGACCAGAGCCTGAAAGG 353
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                                                                               GCTTTTGCAGACCGCGGTCCTGCAGGGGCGCTTGCTGCGTTCACACTCTCTGCACTACCT
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230846 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF080089
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PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 48 row: E column: 9
Seq primer: ATTTAGGTGACACTATAG.
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Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch al Similarity 73.1%; Pred. No. 7.5e-61; 356; Conservative 0; Mismatches 107;
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                                                                                                                                                                                                                                                                /organism-"Mus musculus"
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1. .489
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                                                                                                                                                                                                                                                                               /strain="C57BL/6
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                                        20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                               /note="Vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
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                                                                                                                                                                                                                                                                                                AGAAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGAAATGGGCCCCGCGAGCCAG 238
                                                                                                                                                                                                                                                                                                               62 AGCGGCCGAAAAGCACCTGGAAGCGCGGTCCGAGCC--GGGAAATGGGCCCACAAACCCG 119
                                                                                                                                                                                                                                                                                                                                                     GCCGCCCTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTGCAGGGGCGCTTGCTGCG 298
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                                                                                                                                                                                          Length 523;
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Pred. No. 1.2e-65;
0; Mismatches 110;
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97044477
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/tissue_type="pooled"
/lab_host="DHIOB"
     Location/Qualifiers
1. .523
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Best Local Similarity 74.0%;
Matches 387; Conservative (
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/clone="UI-M-CGOp-bix_Ret4_S2"
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TAG_SEQ_None found"
                                                                                                                       coligo-dT track not found.

15 likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: Researchers may obtain BMAP cDNA

clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized

non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The following repetitive elements were found in this cDNA sequence:
11-31, >(CAG)n#Simple_repeat
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GCTACTGGAAGTACGGGTATGATGGCCAGGACCACCTTGAATTCTGCCCTGACACACTG 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus mus/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                        445 AACATCACTATGA 457
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/db_xref="taxon:10090"
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/lote="vector: p7733-pec (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; The
NIH_BMAP_MSC library is a non-normalized library
constructed from mouse spinal cord. The tag is a string
of 5 nucleotides present between the Not I site and the
oligo-dr track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
/lygo-dr Lissue provided by Ms. Annie Novakovich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH etermines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: Seq primer: M13 Forward
                                                                                                                              AI850020 457 bp mRNA linear EST 15-JUL-1999 UI-M-BGO-aib-g-10-0-UI.S1 NIH_BMAP_MSC Mus musculus cDNA clone UI-M-BGO-aib-g-10-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I toases 1 to 457, Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
78292-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
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Pred. No. 4.4e-59;
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TAG_TISSUE-spinal-cord
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 301 443 9890
Email: mEST@mail.nih.gov
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79.6%;
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AUTHORS
TITLE
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Fig. 2014.95 30.00 to 10 in the control of sequence object of track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this CDNA sequence: 1-31, >(CAG)n#Simple_repeat
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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polylinker: Site_l: Not I; Site_2: Eco RI: The
NIH_BMAP_REt4_S2 library is a subtracted library,
145 GGCTTCTGGAGATATGGTTATGACGGCCAAGATCACCTGGAATTCTGCCCCAAGACACTA 204
                                                                                                                                              205 AACTGGAGCGCAGCCGAGCCAGGGCCTGGGCCACCAAGGTGGAATGGGACGAGCAAGG 264
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
TH: 301 443 1706
Fax: 301 443 9890
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/dev_stage="4 weeks"
/lab_host="DH10B"
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|larity 74.1%;
|Conservative
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 06-FEB-1997
                                                                                                                                                                             ö
ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.ulowa.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MUB9b05.rl Soares mouse lymph node NbMLN Mus musculus cDNA clone IMAGE:652689 5' similar to TR:G940354 G940354 CLASS I HISTOCOMPATIBILITY ANTIGEN-LIKE PROTEIN: ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:398537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         681 GATTGGAGGAGCAGCAGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAG 740
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                                                                                                                                                                                                                                                                                              561 GAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAG 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                               ;
0
                                                                                                                                              Score 248.4; DB 10; Length 455; Pred. No. 3e-58;
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                                                                                    83 t
                                                                                                                                                                               0; Mismatches
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The WashU-HHMI Mouse EST Project
                                                                                    144 g
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AA217236.1 GI:1826237
                                                                                                                                                17.2%;
al Similarity 79.5%;
294; Conservative
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Fax: 314 286 1810
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Matches 29
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AA217236/c
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268 bp mRNA linear EST 20-AUG-1996 zb51906.rl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307162 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                           /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570 ACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGG 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAGA 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 464;
Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham. Location/Qualifiers
                                                                                     /strain="C57BL/63"
/db_xref="taxon.10090"
/clone="ImAGE:652689"
/sclone=lib="Soares mouse lymph node NbMLN"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 230; DB 9; Length 464
Pred. No. 4.2e-53;
0; Mismatches 90; Indels
                                                                                                                                                                              /tissue_type="lymph node
                                                                          /organism="Mus musculus"
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Bovoidea;

us-09-497-957-12.rst

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Email: smith@email.marc.usda.gov
single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                1 (bases 1 to 546)
Smith.T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.E., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
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                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel.
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
214520 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 214.6; DB 1
Pred. No. 9.2e-49;
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139 c 180 g 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORMARD: AGGAACAGCTATGACCAT
BACKMARD: GTTTTCCCAGTCACGACG
Plate: 71 row: A column: 5
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                   BE809138.1 GI:10240250
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85.9%;
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/organism="Homo sapiens"

/organism="Homo sapiens"

/db_xref="dbB:1250574"

/db_xref="taxon:0506"

/clone="lb="Soares_fetal_lung_NbHL19w"

/dev_stage="19 weeks"

/dev_stage="10 wee
                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 268)

1 (bases 1 to 268)

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded CDNA was size selected, ligated to ECO RI adapters (Pharmacia), digested with Not I and cloned into the Not I and ECO RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbH13W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1642 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1201 TAATATTAAGGAAGAGGCAGGGTTCAAGAGGAGCCATGGGGGCACTACGTCTTAGCTGAAC 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1261 GTGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGAAAACTAGAGACTCAAAG 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1321 AGGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGGAGAACCTAAACATAGAAAT 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 GTGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAACTAGAGACTCAAAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 AGGGGGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGTTGAACCTAAACATAGAAAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 268;
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0; Mismatches 1;
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                                                       561 GAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAG 620
                              Gaps
                                                                                                                                                                                     741 ATTCGGGCCAGGCAGAACAGGGCCCTACCTGGAGGGAGCTGCCCTGCACAGCTGCAGCAG
                                                                                                                                                                                                                                             GGCTACTGGAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACTG
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Length 546;
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174 CCAAAAGAAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGAAATGGGCCCGCGA 233
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/dev_stage="7 months"
/lab_host="DH108"
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/db_xref="taxon:10090"
/clone="INAGE:2249395"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 ATCATGGGCAACTATAACCACAGTAAGG 449
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TITLE
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                                                                                                                      234
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                  Mammalia; Butheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases I to 481) Atamura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Arimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Y., Tto, M., Rawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Y., Tto, M., Rawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Okazaki, R., Okazaki, Y., Okido, T., Saito, R., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Tayawa, Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carinci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
Carinci,P., Shibata,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                          BB851691 RIKEN full-length enriched, B16 F10Y cells Mus musculus CDNA clone G370002P09 5', mRNA sequence.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Vokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical Archive (RIKEN)
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/orqanism="Mus musculus"
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/clone="G370002P09"
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BI452668 831 bp mRNA linear EST 21-AUG-2001 603169877F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5249395 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Latting in institute of institution of institution in the contact: Robert Strausberg, Ph.D.
Tissue procurement: Lothar Hennighausen Ph.D., Robin Humphreys on Itssue procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAMI1629 row: j column: 20
High quality sequence stop: 818.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 831)
I (bases 1 to 831)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Email: genome-reségac.riken.go.jp,
URL:http://genome.gac.riken.go.jp,
Carninol.p., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
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encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, B16 F10v cells"
/cell_type="B16 F10v cells"
139 c 147 g 118 t
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/clone="G370049A15"
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llarity 67.8%;
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Tto, M., Kawal, J., Kojima, Y., Kondo, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akhaira, S., Tanaka, T., Tomaru, H., Tagawa, Watahiki, A., Yasanishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB858165 RIKEN full-length enriched, B16 F10Y cells Mus musculus CDNA clone G370049A15 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                          1055 GAGATATACGTACCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGA 1114
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                                                                                17;
                                 Length 831;
                                                                                Indels
                               DB 10;
                                                                           Mismatches 143;
                               Score 202.2; DB 1
Pred. No. 3.3e-45;
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Length 502; Indels

Search completed: June 19, 2002, 07:21:51 Job time: 2597 sec

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June 19, 2002, 08:49:52 ; Search time 352.95 Seconds (without alignments) 7004.836 Million cell updates/sec
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1440
1 GGGGACACTGGATCACCTAG:.....TCCTCAAAAGATTTCCCCA 1440
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A. Ceneseq. 0.4280.1:*

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3. SIDS1/gcgdata/geneseq/geneseqn.embl/NA1981.DAT:*

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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES 8		Description	Human boroditary	Human horoditary n	Human hereditary h	Hereditary haemoch	Human hereditary h	Hapmontomatoria a	CONSTRUCTION OF STRUCTURE OF ST	Human polynucleoti	Human hereditary h
		ID	AAC68432	AAC68430	AAC68431	AAT96691	AAC68429	AAV23525	AAA96769	AA163897	AAC68427
	Query	DB	22	22	22	18	22	19	21	22	22
		Match Length DB	1440	1440	1440	1440	1440	2727	2506	596	10825
		- 1	100.0	6.66	6.66	8.66	8.66	8.66	84.4	38.7	22.3
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      Tsuchihashi
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Pred. No. 0;
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         Gnirke
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Best Local Similarity 99.9%;
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This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmid-based cDNA library following identification of the HH locus in the HLA region of chromosome 6. A single mutation (24d1) in the HH gene a ppears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. It results in a critical disulphide bridge important for secondary structure. The collowing are claimed: a 10825 bp genomic DNA sequence (I) (see AAP96690), the 1437 bp cDNA sequence (Ia) and their 24d1, 24d2 and collowing are claimed: a 10825 bp genomic DNA sequence (I) (see AAP96690), the 1437 bp cDNA sequence (Ia) and their 24d1, 24d2 and 24d7, oar appetide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method mutation; an annial model for the HH disease; metal chelation agents, T-cell differentiation factors and therapeutic agents for the mitigation of injury due to oxidative process in vivo or inigiation of injury due to oxidative process in vivo or the harmannest; and the presence or an enthod or contential annity for annity the presence or metation of injury due to oxidative process in vivo or the harmannest or the mitigation of injury due to oxidative process in vivo or the harmannest or the har
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hereditary haemochromatosis gene and variants - useful for diagnosis and treatment of hereditary haemochromatosis disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for HH homozygotes, to HH diagnosis, prenatal screening and diagnosis, and therapies of HH disease, including gene therapy, protein- and antibody-based therapeutics, and small molecule
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/note= "G to A substitution (24d1 mutation
associated with HH), results in Cys
Tyr substitution"
                             A to T substitution (24d7 variant) results in Ser to Cys substitution"
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96US-0632673.
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Z, Wolff RK;
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04-APR-1996;
16-APR-1996;
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Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;

ö Length 1440; ; 2; Indels DB 18; Score 1436.8; Pred. No. 0; 0; Mismatches ; 0 99.88; Matches 1438; Conservative Local Similarity Query Match

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120 180 300 300 360 360 TIGAAGCTITGGGCTACGIGGAIGACCAGCTGTTCGTGTTCTATGAIGAGAGTCGCC 420 420 480 540 540 900 900 99 720 gtgtggagccccgaactccatgggtttccagtagaatttcaagccagatgtggctgcagc 480 099 900 61 ACTAAAGTICIGAAAGACCIGITGCITITICACCAGGAAGITITIACIGGGCAICTCCIGAG CCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCCGTTTCCCCGGCCCCCCAAAAG AAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGGAAATGGGCCCGCGAGGCCAGGC CGGCGCTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTGCAGGGGCGCTTGCTGCGTT CACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGT GTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGC AATTCTGCCCTGACACACTGGATTGGAGCAGCAGCAGAACCCAGGGCCTGGCCCACCAAGC aattetgeeetgacacactggattggagagcagcagaacccagggcetggeecaaage 841 ctcctttggtgaaggtgacacatcatgtgacctcttcagtgaccactctacggtgtcggg TGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGG 541 AAAATCACAACCACAGGAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGC AAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGGGCAGGACCACCTTG CCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGG ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCT GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGCACC TGGAGTGGGAAAAGCCACAAGATTCGGGCCAGGACAGGGCCTACCTGGAGAGGGGCT GCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGGGTGTTTTGGACCAACAAGTGC 841 CTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGG 121 241 181 241 301 301 361 361 121 421 481 181 601 601 661 661 721 721 781 1081 1081 901 901 961 1021 δ g g οp Dp ò δ δ δ a ò d ò g ò g ŏ g g g ŏ ŏ a ŏ δ g δŽ Dp g δλ ò pp g a δ

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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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96US-0652265.
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                                                                 CCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCCGGTTTCCCCGCCCCCAAAAG
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         CACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGT
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                                 ACTAAAGTTCTGAAAGACCTGTTTGCTTTTCACCAGGAAGTTTTACTGGGCATCTCCTGAG
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Indels

Length 1440;

DB 22; 5;

Score 1436.8; Mismatches No. 0;

Pred.

99.88;

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Conservative

Local Similarity tes 1438; Conserv

Best Loca Matches

Query Match

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This sequence represents the haemochromatosis (HC) gene. Mutations in this sequence are detected using the method of the invention. The method is for identifying an individual with hereditary haemochromatosis (HH) or a predisposition to develop HH or to genetically pass on HH to an offspring, comprising isolating a biological sample and amplifying a coffspring. Comprising isolating a biological sample encompassing all or part of the DNA between markers D6265 and D6276, and detecting at least one homozygous or heterozygous mutation in a nucleotide within the region. The method can also be used for identifying an individual with an autosomal recessive discorder (ARD) or predisposition to develop and/or genetically pass on an ARD to an offspring, comprises isolating a biological sample from the individual and screening genomic DNA in the sample for the presence of a homozygous or heterozygous mutation in a
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                                                                       TAATATTAAGGAAGAGGCAGGGTTCAAGAGGAGCCATGGGGCCACTACGTCTTAGCTGAAC
                                                                                                                                          taatattaaggaagaggcagggttcaagaggagccatggggcactacgtcttagctgaac
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                                                        TIGGAGICATCAGGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTGTTCA
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gene, the normal function of which, is required to prevent progression of the disorder. The method(s) can be used to identify individuals that are homozygous or heterozygous (carriers) for the mutation causing the ARD. Especially the method is used to diagnose HH or predisposition to HH by detecting a Cys282Tyr substitution. Individuals homozygous for this mutation have HH and heterozygotes are potential carriers of the
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/product= "histocompatibility iron loading (HFE) protein"
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                                                                                                                                                                                                                                                                                                                                                                 sequence encoding a histocompatibility iron loading (HFE) protein
                                                                                                                                                                                                           1081 caggectggatcagececteattgtgatetgggageeetcacegtetggeaeectagtea 1140
                                                                                                                                                                                                   GTGAGTGACACGCAGCCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAAG 1320
                                                                                                          CAGGCCTGGATCAGCCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCA 1140
                                                                                                                                       ITGGAGTCATCAGTGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTGTTCA 1200
                                                                                                                                                1201 TAATATTAAGGAAGAGGCAGGGTTCAAGAGGAGCCATGGGGGCACTACGTCTTAGCTGAAC 1260
                                                                                                                                                                                                                                                                        ctcctttggtgaaggtgacacatcatgtgacctcttcagtgaccactctacggtgtcggg
                       961 ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCT
                                                                           GGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGCACC
                                                                                                                                                                                                                                                                TGCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCA
                CCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "if this base is mutated to T, then the protein contains the mutation S65C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                               HFE protein;
class I gene;
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G93R"
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/note= "if this base is mutated to G, i
protein contains the mutation ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       if this base is mutated to C, protein contains the mutation
                                                                                                                                                                                                                                                                                                                                                                               Human; histocompatibility iron loading protein; major histocompatibility complex; non-classical chromosome 6p; iron disorder; haemochromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                     standard; cDNA; 2506 BP
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e.g. haemochromatosis, or a genetic susceptibility to develop it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation
314
/*tag= f
/note= "if this base is mutated to C, then the
/note= "if this base is mutated to C, then the
protein contains the mutation I105r, which
is associated with an iron overload disorder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutat in exon 2 or an intron of a histocompatibility iron loading nucleic acid.
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Best Local Similarity 99.8%;
Matches 1217; Conservative 0
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cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
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                                                                                                                             ACCACTCTACGGTGTCGGGCCTTGAACTACCCCCCAGAACATCACCATGAAGTGGCTG
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                                                                                     GCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGGAGGT
Human polynucleotide SEQ ID NO 105.
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The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM43467) and seful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The cor ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, c. e.g. breast and ovarian cancer and other cancers of the adrenal gland, cond, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, cautoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Colitis: (c) cardiovascular disorders such as viral, bacterial, fungal cond parasitic infections.

Colitis: (c) cardiovascular disparent did not form part of the princed specification, but was obtained in electronic format directly communication and parasitic format directly communication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATG 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 cccgcccccaaaagaagcggagatttaacggggacgtgcggccagagctggggaaatgg 72
                                                                                                                                                                                                         New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 GCCCGCGAGCCAGGCCGGCGCTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 GGCGCTTGCTGCGTTCACACTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 AIGAIGAGAGTCGCCGIGIGGAGCCCCGAACICCAIGGGIITCCAGIAGAATITCAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 97.6%; Pred. No. 7.4e-152;
Matches 571; Conservative 4; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 105; 664pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 596 BP; 133 A; 157 C; 175 G; 126 T; 5 other;
                                                                                                                   Ruben SM
                                                                             (HUMA-) HUMAN GENOME SCI INC.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
                                                                                                                 Rosen CA, Barash SC,
                                                                                                                                                         WPI; 2001-488781/53.
                                                                                                                                                                         P-PSDB; AAM43591
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3882 gccgtgtggagccccgaactccatgggtttccagtagaatttcaagccagatgtggctgc 3941
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                                                                                                                                                                                                                                                                                                                                            4122 ggagcagggaagagggaaggaatttgcttcctgagatcatttggtccttggggatggtgg 4181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wolff
                                           4062 cagagettttcatettteatgeatettgaaggaaacagetggaagtetgaggtettgtg
                             AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA
                                                                                                                                                                                                                                                                                                                            CACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTG
                                                                                                                                                                                                                                                                                                                                                                                      GAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACTGGATTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                      4362 agcagcagaacccagggcctggcccaccaagctggagtgggaaaggcacaagattcgggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human hereditary hemochromatosis 24d1/2 mutation DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds.
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                                                                                      TGGAAAATCACAACCACAGCAAG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGGGGAGAGGTGTTTTGGACCAACAAG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC68428 standard; DNA; 10825
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96us-0632673.
96us-0652265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-1997;
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23-MAY-1996;
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Feder JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC68428;
                                                                                                                  4002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iron overload. They may also be used in protein replacement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3762 gttcacactctctgcactacctcttcatgggtgcctcagagcaggaccttggtctttcct 3821
              705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      individuals having a defective human hemochromatosis gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a parient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for
                     GGCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.3%; Score 321; DB 22; Length 10825; 72.1%; Pred. No. 2.2e-82; ive 0; Mismatches 0; Indels 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 other;
                                                              Human hereditary hemochromatosis 24d2 mutation DNA

    hereditary hemochromatosis; chelation agent;
    cell differentiation factor; iron overload; ds

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                      AAC68427 standard; DNA; 10825 BP
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96US-0632673.
96US-0652265.
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                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIRA ) BIO-RAD LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-006341/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB36871.
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-1997;
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23-MAY-1996;
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                                                                                                                                                                                                   AAC68427;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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4482 gctggggagaggtgttttggaccaacaag 4510
                                                                                                                                   Hereditary haemochromatosis gene.
                                                           AAT96690 standard; DNA; 10825
                                                                                                           (first entry)
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                                                                                                                                                                                              Homo sapiens
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                                                                                                                      products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4122 ggagcagggaagaggaaggaatttgcttcctgagatcatttggtccttggggatggtgg 4181
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                                                                                                                                                                                                                                                                                298 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357
                                                                                                                                                                                                                                                         Gaps
                                    New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  629 GAAGTACGGGTATGATGGCCAGGACCACCTTGAATTCTGCCCTGACACTGGATTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569 CACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTG
                                                                                                                                                                                                                                                                                                                                                                               GCCGTGTGGAGCCCCGGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
                                                                                                             The present invention relates to hereditary hemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                           Indels 209;
                                                                                                                                                                                                                                Length 10825;
                                                                                                                                                                                             Sequence 10825 BP; 2999 A; 2252 C; 2648 G; 2926 T; 0 other;
                                                                                                                                                                                                                                Score 321; DB 22;
Pred. No. 2.2e-82;
0; Mismatches 0;
                                                             chelation agent alleviating iron overload
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                                                                                     Disclosure; Fig 3; 108pp; English.
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72.1%;
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             P-PSDB; AAB36872
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Hereditary haemochromatosis gene and variants - useful for diagnosis and treatment of hereditary haemochromatosis disease
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"G to A substitution (24d1 mutation
associated with HH), results in Cys to
Tyr substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                       C to G substitution (24d2 mutation) results in His to Asp substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A to T substitution (24d7 variant) results in Ser to Cys substitution"
Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ds.
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Tsuchihashi Z, Wolff RK;
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P-PSDB; AAW36499.
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This genomic DNA sequence corresponds to the human gene whose mutated form is associated with hereditary haemochromatosis (HH).

To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HLA region of chromosome (A physical clone coverage was then generated extending from D65265, which is a marker that is centromeric of that.

CC (HLA-A, in a telemeric direction through D65276, a marker at which can be appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in the HH gene appears responsible for the majority of HH disease. This comprises and in 4% of unaffected chromosomes.

CC (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises and in 4% of unaffected chromosomes.

CC (24d2) in the HH gene appears responsible for the majority of HH disease. This comprises and in 4% of unaffected chromosomes.

CC (24d3) in the HH gene product is secondary attructure. The following are claimed: the HH genomic DNA (1), a structure. The following are claimed: the HH genomic DNA (1), a containts, a cloning or expression vector; host cells; a peptide product chosen from the HH gene product, its variants (24d7 variants, a cloning or expression vector; host cells; a contained by produced using the peptide; a method for case of these; an antibody produced using the peptide; a method containing the peptide; a method containing the peptide; a method for case of the common HH gene mutation; an annimal model for there were appeared of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the product of a nucleic acid sequence due procession product o Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other; Indels Score 319.4; DB 1 Pred. No. 6.4e-82; Mismatches ó: 22.2%; 72.0%; Conservative Similarity therapeutics. Best Local Sim Matches 539; Query Match 3762 3822 358 ò g g á οy

1; 4121 417 298 GTTCACACTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357 477 209; Gaps TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGATGAGAGTC GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA cagagettttcatettttcatgeatettgaaggaaacagetggaagtetgaggtettgtg ggagcagggaagggaaggaatttgcttcctgagatcatttggtccttggggatggtgg ----GAGTCCCA 18; Length 10825; TGGAAAATCACAACCACAGCAAG~ 3942 3882 4002 418 4122 478 538 4062 561 561 561 g Pp δλ qq Ω g ò ò 염 ô

4301 4421 alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene. 4182 aaatagggacctattcctttggttgcagttaacaaggctggggatttttccagagtccca 4241 4481 688 748 Wolff RK; The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for or polypeptides, useful patient, and as a metal CACCCTGCAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTG 689 AGCAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAAAAGGCACAAGATTCGGGC 4362 agcagcagaacccagggcctggcccaccaagctggagtgggaaaggcacaagattcgggc GAAGTACGGGTATGATGGCCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAG 749 CAGGCAGAACAGGGCCTACCTGGAGGGACTGCCCTGCACAGCTGCAGTTGCTGGA Tsuchihashi Z, Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other; I-cell differentiation factor; iron overload; ds hereditary hemochromatosis; chelation agent; New hereditary hemochromatosis gene products for treating hereditary hemochromatosis in a chelation agent alleviating iron overload -Ruddy D, 809 GCTGGGGAGAGGTGTTTTGGACCAACAAG 837 Human hereditary hemochromatosis DNA. Gnirke A, Disclosure; Fig 3; 108pp; English. BP AAC68425 standard; DNA; 10825 96US-0632673. 96US-0632673. 96US-0652265. 97US-0834497 (first entry) (BIRA) BIO-RAD LAB INC Drayna DT, 2001-006341/01. P-PSDB; AAB36869 Homo sapiens. 04-APR-1997; 21-FEB-2001 16-APR-1996; 23-MAY-1996; US6140305-A. 31-OCT-2000 04-APR-1996; Thomas WJ, AAC68425; Feder JN; 269 AAC68425 δy q qq g g ò Qγ g δ à

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16-APR-1996;
23-MAY-1996;
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T-cell differentiation factor; iron overload; ds
      Pred. No. 6.46
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Pred. No. 6.4e-82;
0; Mismatches 1; Indels
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Best Local Similarity 72.0%;
Matches 539; Conservative
97US-0834497
                                                                                                                         (BIRA ) BIO-RAD LAB INC
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                   AGCAGCAGAACCCAGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGC
Human, histocompatibility iron loading protein; HFE protein, major histocompatibility complex; non-classical class I gene; chromosome 6p; iron disorder; haemochromatosis; ss.
                                                                                                                                                           Genomic DNA of a histocompatibility iron loading (HFE) gene.
                                                                             809 GCTGGGGAGAGGTGTTTTGGACCAACAAG 837
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The present sequence represents the human histocompatibility iron loading (HFE) gene. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome op. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number U60319). The presence of the mutation indicates the disorder or the genetic susceptibility to the
                                                                                                                                                                                                                                                                                                       Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorder, The method is used to diagnose an iron disorder
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Pred. No. 6.8e-82;
0; Mismatches 1; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 21-28; 55pp; English
                                                                                                                                                                                    Sawada-Hirai R,
                                                                                                                         (BILL-) BILLUPS-ROTHENBERG INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.2%;
72.0%;
24-MAR-2000; 2000WO-US07982
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The present invention describes hereditary haemochromatosis gene
products from the human haemochromatosis gene. The present sequence
represents a hereditary haemochromatosis subregion from an hereditary
haemochromatosis (HH) affected individual. Also described is a
method to determine the presence or absence of the common hereditary
haemochromatosis (HFE) gene mutation in an individual comprising:
(a) providing DNA or RNA from the individual; and (b) assessing the
DNA or RNA for the presence or absence of a haplotype or genotype where
the presence of the HFE gene mutation in the genome of the likely
presence of the HFE gene mutation in the genome of the individual. The
C HFE gene sequences from the present invention can be used to develop
products for use in the diagnosis and treatment of HFE. The present
Invention also describes BFF genes, which are homologues of the milk
protein butyrophilin (BT), and can be used in the production of agonists
                                                                                                                       Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; ss.
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CAGGCAGAACAGGGCCTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGA
                                            GAAGTACGGGTATGATGGGCAGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAG
                                                                            gaagtacgggtatgatgggcaggaccaccttgaattctgccctgacacactggattggag
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AAV57903 standard; DNA; 237326
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and antagonists of BT function. Also described are: (1) a RoRet gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can similarly be used for hypophosphatemia.
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                                                                                                                                               Length 237326;
                                                                                              Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;
                                                                                                                                          22.2%; Score 319.4; DB 19; 72.0%; Pred. No. 3e-81; ive 0; Mismatches 1; I
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Search completed: June 19, 2002, 08:53:55 Job time: 8120 sec

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APPLICANT: Feder, John N.
APPLICANT: Foirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TILLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY. San Francisco STATE: California COUNTR: USA ZIP: 94111-3834 COMPUTER READABLE FORM:
US-08-724-394A-21

US-08-652-265-21

US-08-652-265-21

US-08-652-265-21

US-08-632-265-21

US-08-632-44A-21

US-08-632-673B-13

US-08-632-673B-3

US-08-632-673B-3

US-08-632-673B-3

US-08-632-673B-3

US-08-632-44A-20

US-08-690-719-5

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                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 17957-000500 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      ; Sequence 12, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
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replace(408, "g")
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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'Cqn2_b/ptodata//ina/5A_COMB.seq:*
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'Cqn2_b/ptodata/1/ina/6A_COMB.seq:*
'Cqn2_b/ptodata/1/ina/6B_COMB.seq:*
'Cqn2_b/ptodata/1/ina/PcTUS_COMB.seq:*
'Cqn2_b/ptodata/1/ina/PcTUS_COMB.seq:*
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           version 4.5
- 2000 Compugen Ltd
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US-08-814-497A-12
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US-08-652-265-11
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US-08-652-265-11
US-08-814-497A-11
US-09-503-444A-9
US-09-503-444A-9
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                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                       383533 seqs, 122816752 residues
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Maximum Match 100%
Listing first 45 summaries
                                                       nucleic search, using sw model
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Copyright (c) 1993
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CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/652,265
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
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COUNTRY: USA
ZIP: 10036-2811
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                           | PEATURE: | NAME/KEY: allale | LOCATION: raplace(1066, "a") | OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis | OTHER INFORMATION: / Iabel= 24d1 | US-08-652-265-18
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APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Beder, John N.
APPLICANT: Glirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: HERDITANT: WOlff, Roger K.
APPLICANT: Wolff, Roger K.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
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STREET: 1155 Avenue of the Americas
CITY: New York
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APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
Sequence 12, Application US/08834497A Patent No. 6140305
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OTHER INFORMATION: /phenotype- "Hereditary
OTHER INFORMATION: /label- 2441
                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-556
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1440; 100.0%; Pred. No. 0;
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                         LENGTH: 1440 base pairs
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Best Local Similarity 100.
Matches 1440; Conservative
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FEATURE:
NAME/KEY: allele
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: allele
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TOPOLOGY: lin
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OTHER INFO
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CTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION:
CTHER INFORMATION: /label= 24dl
US-09-503-444A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1440;
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                    APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Peder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
ATILE OF INVENTION: Hereditary Hemochromatosis Gen
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 3-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1440;
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                        3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- 24d2
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OTHER INFORMATION: /phenoty
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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212-869-9741
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STRANDEDNESS: single
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Best Local Similarity
Matches 1440; Conserv
                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: USA
Patent No. 6228594
GENERAL INFORMATION:
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STREET: 11
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LOCATION:
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                                                     1201 TARTATTAAGGAAGAGGAGGGTTCAAGAGGAGCCATGGGGCACTACGTCTTAGGTGAAC 1260
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                                      TIGGAGICATCAGGGAATTGCTGTTTTTGTCGTCATCTTGTTCATTGGAATTTTGTTCA
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APPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLI
STREET: Two Embarcadero Center, Eighth Floor
TITY: San Emparation
STATE: California
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08652265 Patent No. 6025130 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TINGES, MILESON, APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wilf, Roger K.
TITLE OF INVENTION: Hereditary F.
NUMBER OF SEQUENCES: 44
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
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MEDIUM TYPE: Floppy disk
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LENGTH: 1440 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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STREET: Tw
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LOCATION:
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                                                                                                                    Length 1440;
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   ); LCCATION: replace(1066, "a");
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis;
OTHER INFORMATION: /label= 24d1
US-08-652-265-10
                                                                                                                                                     1; Indels
                                                                                                                    DB 3;
                                                                                                                  99.9%; Score 1438.4; 99.9%; Pred. No. 0;
                                                                                                                                                     0; Mismatches
replace(1066, "a")
                                                                                                                                                     Conservative
                                                                                                                                  Best Local Similarity
Matches 1439; Conserv
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SEQUENCE CHARACTERISTICS:
                                                                                        FEATURE:
NAME/KEY:
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 CCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGG 960
                          1021 GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGCACC
                                                                                         GGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGCACC
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Guirk, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: California
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                                                                                                                                                                                                                                                             Length 1440;
                                                                                                     | COCATION: 222.1268
| FEATURE:
| NAME/KEY: allele
| COCATION: replace(408, "g")
| OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
| OTHER INFORMATION: /label= 24d2
| US-08-652-265-11
                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                            Score 1438.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.9%;
Matches 1439; Conservative
LENGTH: 1440 base pairs
TYPE: nucleic acid
                                single
                                                                                         CDS
222..1268
                                                             MOLECULE TYPE: CDNA
                                              linear
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TOPOLOGY: lin
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            ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCT
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                                                   CTCCTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGG
                                                                                                          CCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGG
GCCCTGCACAGCTGCAGCAGTTGCTGCAGCTGGGGAGAGGTGTTTTGGACCAACAAGTGC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFWWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08834497A
Patent No. 6140305
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: WOlff, Roger K.
TTILE OF INVENTION: HEREDITARY HEMOCI,
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York STATE: New York
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
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                                                                                                                                                                                                                                                                                                                    8907-0056-999
                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILLING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    28,462
                                                                                                                                                                                                                                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,
              04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER:
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                                 CLASSIFICATION:
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GTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGC
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APPLICANT: Feder, John N.
APPLICANT: Galike, Andreas
APPLICANT: Galike, Andreas
APPLICANT: Galike, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HERDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEN: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
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CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-ARR-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POISSAIN, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/POCKET NUMBER: 8907-0056-9
TELECOMMINICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: replace(408, "g")
OTHER INFORMATION: /phenotype= 'OTHER INFORMATION: /label= 24d2
OTHER INFORMATION: /label= 24d2
       Thomas, Winston J.
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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LOCATION: 222..1268
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APPLICANT:
APPLICANT:
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Matches 1439;
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Sequence 11, Application US/08834497A

US-08-834-497A-11

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•	61 ACTAAAGTTCTGAAAGACCTGTTGCTTTTCACCAGGAAGTTTTACTGGGCATCTCCTGAG 120 	121 CCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCGGTTTCCCCGCCCCCCAAAAG 180 	181 AAGCGGAGATTTAACGGGGACGTGCGGCCAGAGCTGGGGAAATGGGCCCGCGAGGCAGGC	CGGCGCTTCTCCTCTGATGCTTTTGCAGACCGCGGTCCTGCAGGGCGCGTTGCTGCGTT 	301 CACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGT 360 	361 TTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGATGAGGGCC 420 	421 GTGTGGAGCCCGAACTCCATGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGC 480 	481 TGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTAITATGG 540	541 AAAATCACAACCACAGGAGTCCCACACCCTGCAGGTCATCCTGGGCTGTGAAATGC 600 	601 AAGAACACAACAGTACCGAGGGTACTGGAAGTACGGGTATGATGGGGGAGGACCACGCTTG 660 	661 AATTCIGCCCTGACACACTGGATTGGAGAGCAGAACCCAGGGCCTGGCCCACAAGC 720 	721 TGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAGAGGGCCTACCTGGAGAGGGCCT 780 	781 GCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGGGTGTTTTGGACCAACAAGTGC 840 	841 CTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGG 900 	901 CCTTGAACTACTCCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGG 960 	961 ATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGAATGGGACTACCAGGGCT 1020 	1021 GGATAACCTTGGCTGTACCCCTGGGGAAGAGGAGATATACGTACCAGGTGGAGCACC 1080 	1081 CAGGCCTGGATCAGCCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCA 1140
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
NUMBER OF SEQUENCES: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WordPerfect Version CURRENT APPLICATION DATA:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows 95
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Avenue of the A
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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STATE: New York
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Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
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Feder, John N.
Gnirke, Andreas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /phenotype= "Hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1438.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                        8907-0088-999
           FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
APPLICATION NUMBER: 08/630,912
APPLING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
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08/652,265
                                                                                                                                                                                                                         TELBEGON.
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SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
                                                                                                                                                       28,462
                                                                                                                                                    REGISTRATION NUMBER: 28,462
REFRENCE/DOCKET NUMBER: 89,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPRAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.9%;
Best Local Similarity 99.9%;
Matches 1439; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: replace(408, OTHER INFORMATION: /phe OTHER INFORMATION: /OTHER INFORMATION: /lab
                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 222..1268
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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LOCATION: replace
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TELEX: 6
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                                                                                                                                                     MEDIDUA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                           ....ureSSEE: Townsend and Crew LLP STREET: Two Embarcadero Center, Elghth Floor STATE: California COUNTRY: USA
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99.9%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEC ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 222..1268
FEATURE: Allele
LOCATION: replace(408, "c")
COTHER INFORMATION: /phonotype= "normal
OTHER INFORMATION: /label= 2462
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(unaffected)"
/label= 24d7
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CTHER INFORMATION: (unaffected)
COTHER INFORMATION: (Label- CT- CS-08-652-265-9
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replace(414, "a")
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 1438; Conservative
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                  CORRESPONDENCE ADDRESS
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OTHER INFORMATION:
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FEATURE:
LOCATION: replace(1
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LOCATION: replace
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                                                                                                                                ZIP: 94111-3834
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                                                                        AGGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAAT
                                                                                                                                                                                                                                                                                           APPLICANT: Feder, John N.
APPLICANT: Galike, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FLING DATE: 04-APR-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORREY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28 462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-ARR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAX-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                   Sequence 9, Application US/08834497A
Patent No. 6140305
                                                                                                                                                                                                                                                                 APPLICANT: Thomas, Winston J. APPLICANT: Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
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222..1268
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                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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LOCATION:
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US-08-834-497A-9
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                    Length 1440;
                                                                                                                                                                                                                        /phenotype= "normal or wild-type (unaffected)" /label= 24d1
                                                                                                                 114, "a")
//phenotype= "normal or wild-type
(unaffected)"
/label= 24d7
                              /phenotype= "normal or wild-type (unaffected)"
/label= 24d2
                                                                                                                                                                                                                                                                                                                                    DB 3;
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                                                                                                                                                                                                                                                                                                                                    Score 1436.8;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                             NAME/KEY: allele

COATION: replace(414, "a")

COTHER INFORMATION: /phenotype=

OTHER INFORMATION: /label= 24d7

FEATURE:

NAME/KEY: allele

LOCATION: replace(1066, "g")

OTHER INFORMATION: /phenotype=

OTHER INFORMATION: /phenotype=

OTHER INFORMATION: /phenotype=

OTHER INFORMATION: /label= 24d1

US-08-834-497A-9
NAME/KEY: allele
LOCATION: replace(408, "c")
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: /label= 24
FEATURE:
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Best Local Similarity
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                                                                           721 TGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCCAGAACAGGGCCTACCTGGAGAGGGACT
                                                            781 GCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGGGTGTTTTGGACCAACAAGTGC
                                                                                                                        841 CTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTCGGG
                                                                                                                                                                                                                                                             APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Peder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Woger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09503444A Patent No. 6228594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
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/label= 24d2
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(unaffected)"
/label= 24d7
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/label= 24d1
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                                                                                                                                                                                                                                                                                                                                                              8907-0088-999
                                                    APPLICATION NUMBER: US/09/503,444A FILLING DATE: 14-Feb-2000 CLASSIFICATION:
                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
APPLICATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-00!
TELECHANICATION INFORMATION:
TELECHANICATION FOR SQL ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH:
                8
              SOFTWARE: WordPerfect Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows 95
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OTHER INFORMATION: /phenotyr
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OTHER INFORMATION: /label= ;
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Matches 1438; Conservative
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STRANDEDNESS: single
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LOCATION: 222..1268
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US-09-277-457-1
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      CGGCGCTTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTGCAGGGGCGCTTGCTGCGTT
             CACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTGT
                                            TTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGAGAGTCGCC
                                                                         GTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGCCTGCAGC
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180 461 240 300 281 341 120 401 521 581 360 641 420 701 480 540 761 Gaps 9 222 ATGGGCCCGCGAGCCAGGCCGGCGTTCTCCTCATGCTTTTGCAGACCGCGGTCCTG GACCTTGGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTC TATGATGATGAGAGTCGCCGTGTGGAGCCCCGAACTCCCATGGGTTTCCAGTAGAATTTCA agccagatgtgggctgcagctgagtcagagtctgaaagggtgggatcacatgttcactgtt GACTTCTGGACTATTATGGAAAATCACAACCACAGCAAGGAGTCCCACCCCTGCAGGTC gaettetggaetattatggaaaatcacaacacacaggaaggagteccacacectgcaggte atcctgggctgtgaaatgcaagaagacaacagtaccgagggctactggaagtacgggtat AGCCAGATGTGCCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTT ATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTAT GATGGGCAGGACCACCTTGAATTCTGCCCTGACACTGGATTGGAGAGCAGCAGAACCC AGGGCCTGGCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGG TGCCTGACGAACTCCTTGATTTTAGCCTTCTCTGTTCATTTCCTCAAAAAGATTTCCCCA 2506; 0; DISORDERS Length Indels 314 nucleotide 4; IRON 2, APPLICANT: Rothenberg, Barry E.
APPLICANT: Sawada-Hiral, Ritsuko
APPLICANT: Sawada-Hiral, Ritsuko
APPLICANT: Barton, James C.
TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRC
FILE REPERENCE: 10653/002001
CURRENT APPLICATION UNBER: US/09/277,457
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0 DB Score 1215.8; Pred. No. 0; 0; Mismatches NAME/KEY: mutation
LOCATION: (0)...(0)
COTHER INFORMATION: Missense mutation at
US-09-277-457-1 Sequence 1, Application US/09277457 Patent No. 6355425 GENERAL INFORMATION: 0; 84.48; 99.88; Conservative ORGANISM: Homo Sapiens Best Local Similarity Matches 1217; Conserv

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US-08-652-265-5
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                                                                                                                                                                                                                                                          GATGGGACCTACCAGGCCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATAT 1061
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                                                                                                                                                                                          AAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGG 1001
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                                                                                ACCACTCTACGGTGTCGGGCCTTGAACTACCCCCGAGAACATCACCATGAAGTGGCTG 941
                                                                                                                                                            661 accactctacggtgtcgggccttgaactactccccagaacatcaccatgaagtggctg 720
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                                                               GTTTTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTG
                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, Dennis T.
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Hereditary Hemochromatosis Gene
NUMBER OF INVENTION: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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298 GTICACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 357
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OTHER INFORMATION: /product="Hereditary Hemochromatosis OTHER INFORMATION: mutation"

OTHER INFORMATION: /note="Hereditary Hemochromatosis OTHER INFORMATION: gene 24d2 allele"

FEATURE:
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 2442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic sequence surrounding variant for 24d1(G) allele (SEQ ID NO:20)"
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
                                                                                                                              FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 3852..3891
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LOCATION: 5507..6023
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OTHER INFORMATION:
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Best Local Similarity
Matches 540; Conserv
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LOCATION:
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                                                     4062 CAGAGCTTTTCATCTTTTCATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTG 4121
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirk, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Reger K.
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
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STREET: Two Embarcadero Center, Eighth Floor
TITY: San Francisco
STATE: California
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                                   TGGAAAATCACAACCACAGCAAG-----
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Patent No. 6025130
GENERAL INFORMATION:
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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3762 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCT 3821
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                                                                                                                                                                                                                                                                                                                    LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: and 24d2 mutations"

OTHER INFORMATION: /note= "Hereditary Hemochromatosis OTHER INFORMATION: /pote= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: /pote containing a combination of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.3%; Score 321; DB 3; Length 10825; 72.1%; Pred. No. 4.8e-83; Live 0; Mismatches 0; Indels 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COTTION: Teplace(5834, "a")
COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d1
US-08-652-265-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                            and 2462 mutations"
/note= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
2461 and 2462 alleles"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "start and stop positions for
genomic sequence surrounding variant
for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
REFERENCE/DOCKET NUMBER: 17957-000500 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= 24d2
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OTHER INFORMATION: /phenotvop
                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72.1
Matches 540; Conservative
                                                                                                                                                                                                           single
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OTHER INFORMATION: /r
OTHER INFORMATION: 96
OTHER INFORMATION: fc
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: replace
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Unclassified.
1 (bases 1 to 10825)
Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D., Tsuchihash, Z. and Wolff, R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 1 31-OCT-2000;
Location/Qualifiers
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Sequence 1 from patent US 6140305.
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Copyright (c) 1993 - 2000
                                                                              nucleic search, using sw model
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Maximum Match 100%
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1 (bases 1 to 10825)

Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 7 31-OCT-2000;
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Similarity 100.0%; Pred. No. 1.2e-76;
O: Mismatches 0;
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2252 c 2649 g
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 3 31-OCT-2000;
Location/Qualifiers
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1 (bases 1 to 10825)

1 rhomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuchihashi, Z. and Wolff, R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 1 08-MAY-2001;
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                                                                   Score 301; DB 6;
Pred. No. 1.2e-76;
Mismatches 0;
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         /organism="unknown"
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Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuchihashi, Z. and Wolff, R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 3 08-MAY-2001;
Location/Qualifiers
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61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC
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100.0%; Score 301; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 301; Conservative 0; Mismatches 0;
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Sequence 3 from patent US 6228594
AR149460.1 GI:15114051
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ORGANISM

REFERENCE AUTHORS BASE COUNT

ORIGIN

JOURNAL

TITLE

FEATURES

121

61

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181

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/db_xref="SWISS-PROT:030201"
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STEALGYVDDQLFVPYDHESRNVEPFPWVSSTISSQMWLQLSOSIKGWDHWFTVDF
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RAWPTKLEWBRHKIRARQNRAYLERDCPAQLQOLLELGRGVLDQQVPPLVKYTHHVTS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Albig,W.
Direct Submission
Submitted (14-MAR-1997) Albig W., Georg-August-Universitaet
Goettingen, Blochemie und Molekulare Zellbiologie, Humboldtallee
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Albig,W., Drabnt,B. Burmester,N., Bode,C. and Doenecke,D. The haemochromatosis candidate gene HFE (HLA-H) of man and located in syntenic regions within the histone gene cluster J. Cell. Blochem. 69 (2), 117-126 (1998)
                                                                                                                                                                                                                                                                                     241 AATGTCAAGGCCGGGCACGGTGGCTCACCCTGTAATCCCAGGACTTTGGGAGGCCGAGG
4690 CACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGGAAGTGCTATG
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                                                          TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC
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/note="haemochromatosis candidate gene"
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/clone_lib="ICRF YAC-library"
1028. 1324
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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Location/Qualifiers
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/gene="HFE"
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KEYWORDS
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                                                            1 (bases 1 to 10825)
Thomas W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Thomas W.J., Drayna, D.T.,
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
hemochromatosis gene mutation
Patent: US 6228594-A 5 08-MAY-2001;
Location/Qualifiers
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( bases 1 to 10825)

Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D., rsuchihashi, Z. and Wolff, R.K.

Tsuchihashi, Z. and Wolff, R.K.

Tsuchihashi, S. or determining the presence or absence of a heredith hemochromatosis gene mutation
Patent: US 6228594-A 7 08-MAY-2001;
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100.0%; Pred. No. 1.2e-76;
Live 0; Mismatches 0;
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100.0%; Score 301; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.2e-76;
Matches 301; Conservative 0; Mismatches 0;
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AR149462
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Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
Thomas,W., Tsuchhihashi,Z. and Wolff,R.K.
Megabase transcript map: novel sequences and antibodies thereto
Patent: US 5872337-A 20 16-FEB-1999;
Location/Qualifiers
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AR036573.1 GI:5953241
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Sequence 20 from patent US 5872237.
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Feder, J.Nathan., Kronmal, G.Scott., Lauer, P.M., Ruddy, D.A.,
Thomas, W., Tsuchihashi, Z. and Wolff, R.K.
Megabase transcript map: novel sequences and antibodies thereto
Patent: US 5872237-A 21 16-FEB-1999;
Location/Qualifiers
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Feder, J.Nathan., Krommal, G.Scott., Lauer, P.M., Ruddy, D.A.,
Thomas, W., Tsuchihashi, Z. and Wolff, R.K.
Megabase transcript map: novel sequences and antibodies thereto
Patent: US 5872237-A 22 16-FEB-1999;
Location/Qualifiers
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                                                                        AUTHORS
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246282)
14 (bases 1 to 246282)
15 (bases 1 to 246282)
16 (bases 1 to 246282)
17 (bomingo, R. Jr., Meyer, N.C., Irrinki, A., McClelland, E.E., Fullan, A., Moningo, R. Jr., Meyer, N.C., Irrinki, A., McClelland, E.E., Fullan, A., Mapa, F.A., Moore, T. Thomas, W., Loeb, D.B., Harmon, C., Tsuchihashi, Z., Wolff, R.K., Schatzman, R.C. and Feder, J.N.

A 1.1-Mb transcript map of the hereditary hemochromatosis locus
                                                                                                                                                                                                                                                                                                                                                                                                                OY 241 AATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCCGAGG 300 197113 AATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGAGG 197172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.
                                    196933 IGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 196992
                                                                                                                                                                                                                                                                                                          DD 197053 GCCCTTGCTTTTATTTAACCAATAATCTTTTGTATATTATACCGTGTTAAAAATTCAGA 197112
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Ruddy, D.A., Kronmal, G.S., Lee, V.K., Mintier, G.A., Quintana, L., Domingo, R. Jr., Meyer, N.C., Irrinke, A., McClelland, E., Fullan, A., Mapa, F.A., More, T., Thomas, W., Loeb, D.B., Harmon, C., Direct Submission.

By Control Submission (26-FEB-1997) Sequencing, Mercator Genetics, 4040

Campbell Avenue, Menlo Park, CA 94025, USA

Location/Qualifiers

1. 246282

Location/Qualifiers

1. 246282
                                                                                                                                                                       Db 196993 CACAAGTCATGGGTTTAATTTCTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATG 197052
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61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193752)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk
on Aug 27, 2000 this sequence version replaced g1:9864230.
                                                                                                                                                                                                                                                                               61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
                                                                                                                                                                                                                                                                                                                                                      121 CACAAGTCATGGGTTTAATTTCTTTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATG 180
                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATTTTATACCTGTTAAAAATTCAGA 240
                                                                                                                                                                                                       1 GCCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTCTCCAAATTC 60
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                                                                                                                                       Length 246282;
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Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 18325 bases at least Q40 consensus quality: 189768 bases at least Q20 lnsert size: 192052; sum-of-contigs insert size: 192052; sum-of-contigs insert size: 198247; agarose-fp
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                                                                                                                                   Score 301; DB 9;
Pred. No. 1.4e-76;
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Contact: humquery@sanger.ac.uk
Project Information
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AL359892.5 GI:9930971
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67743. 68016
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100.0%;
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AUTHORS
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NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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59845: contig of 2389 bp in length
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43490: con
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/number=6
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/number=4
1995. .2108
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/number=2
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/number-3
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Diceros blocnis.

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Diceros.

I (Dases I to 4349)

West.(C.J., Worley,M. and Beutler,E.

Rhinoceros HFE Polymorphisms
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64073. .82711

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fragment_chain:3"

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Pred. No. 4.1e-76;
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99.7%;
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2 (bases 1 to 4349)
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/db_xxef="Laxon:9805"
join(<1. .264,468. .743,1588. .1863,1995. .2108,3109. .>3149)
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                                                                                                                                                                                                                                                                                                                     .3149)
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West,C.J., Worley,M. and Beutler,E.
Direct Submission
Submitted (30-MG-2000) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2108,3109.
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/codon_start=3
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Pred. No. 2e-15;
0; Mismatches 37;
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AA573540 nf41b05.s
A1732239 nf41b05.x
A1732239 nf35f10.x
AG144127 Pan trog1
AG08435 Pan trog1
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AV713396 AV713396
AA720754 nv93g11.r
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B1522662 603175686
B1906585 603064226
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 531)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                     BG257716 602377406
BC008448 Homo sapi
BG054544 7045112.x
AQ228137 HS_2014_B
BM423178 PLATES_C0
AQ210277 HS_3249_B
AQ475579 CITBI EL-
                                                                                                                                                                                                                                                                                                                                          AQ703007 531 bp DNA linear GSS 07-JUL-1999 HS_5443_B1_G09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1019 Col=17 Row=N, DNA sequence.
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AF113008 Homo sapi
BE14774 RC1-HT022
AQ26902 RPCI11-74
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AG095800 Pan trog1
                                                                             F25183 HSPD12013 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
Oniversity of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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Plate: 1019 row: N column: 17
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Class: BAC ends
                    AG061477
AF113008
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AG090274
AG095800
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 June 19, 2002, 08:24:43 ; Search time 1700.16 Seconds (without alignments) 2389.530 Million cell updates/sec
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AG019823 Homo sapi
AG020621 Homo sapi
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AQ471624 CITBI-E1-
AZ475685 ew02e08.x
AQ15685 ga38607.x
AQ150673 HS_3203_A
AW020486 df10e08.y
AM020486 df10e08.y
AN1565873 tq49q04.x
BF898122 RCI-MT016
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H71349 yu55h06.s1
N58729 yv74a10.s1
AQ489145 RPCI-11-2
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                                                                                                                      1 GGCACGGAATCCCTGGTTGG.......GCACTTTGGGAGGCCGAGGC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                           27472414
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                     13736207 seqs, 6748477542 residues
                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                  US-09-497-957-3_COPY_4570_4870
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Maximum Match 100%
Listing first 45 summaries
                                           - nucleic search, using sw model
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62.22.22.88.88
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Result Š

Searched:

Sequence: Perfect

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659 bp DNA linear GSS 19-OCT-1999 genomic DNA, 21q region, clone: B266G18_SpN017_Rv,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 CTATGGCCCTTGCTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAAAAAT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 CAAAGAGCTATATTTACTATATGACCAGAAAATTTAAAGTCATTGCAACCTTTAAAAAA 140
                                                                                           176 CTATGGCCCTTGCTTTTATTTAACCAATAATCTTTTGTATTTTATACCTGTTAAAAT 235
                                                                                                                                                      Length 630;
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Pred. No. 2.6e-06;
0; Mismatches 38;
                               Score 65.2; DB 12;
Pred. No. 2.6e-06;
0; Mismatches 38;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/clone="b266G18_spN017_Rv"
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genomic survey sequence
AG020621
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69.8%;
                               21.7%;
ilarity 69.8%;
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Matches 88; Conserv
                                                 Similarity
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Best Local S.
Matches 88
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/db_xref="taxon:9606"
/clone="Plate=1019 Col=17 Row=N"
/clone="lba"RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1 = conRibration of EcoRI
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

a 114 c 146 g 137 t 5 others
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Homo sapiens genomic DNA, 21g region, clone: B2289H10 SpN077(-21),
genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-0021-1999) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, RIKEN Genomic Sciences Center(GSC) c/o Kitasato University; 1-15-1 Kitasato, Sagamihara 228-8555, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:042-778-9923, Fax:042-778-9924)
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                  443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTCTCCCAAATTC 323
                                                                                                                                                                                                                                                                                                                                  61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
                                                                                                                                                                                                                                                                                                                                                                                            121 CACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATG 180
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Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,
Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA, Arcamosome 21q
Published Only in DataBase (1999) in press
2 (bases 1 to 630)
Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,
Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                     Score 260.2; DB 12; Length 531;
Pred. No. 2.7e-55;
0; Mismatches 5; Indels 0;
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    630
    /organism="Homo sapiens"
/db_xref="taxon:9606"

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Best Local Similarity 98.1%;
Matches 262; Conservative
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Best Local Similarity 70.8
Matches 85; Conservative
                                                                                               mRNA sequence.
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E. 1 (Dases 1 to 422)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman, M., Hullman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soaces,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The Washur Merck EST Project

Unpublished (1995)

Contact: Wilson RK
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810
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/organism="Mono sapiens"
/db_xref="GDB:1259067"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="lib="soares_parathyroid_tumor_NbHPA"
/clone="lib="soares_parathyroid_tumor"
/clone="tayon="parathyroid tumor"
/dev_stage="adult"
/dev
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                                                                   EST 10-0CT-1996
                                                                                            zc05d01.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
IMAGE:321409 5' similar to contains Alu repetitive element; , mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length; 597 Std Error: 0.00
Seg primer: mob.REGA+ET
High quality sequence stop: 350.
Location/Qualifiers
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Pred. No. 2.9e-06;
0; Mismatches 20; Indels
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Best Local Similarity 79.4%;
Matches 77; Conservative
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 533)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
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CITBI-E1-2590621.TR CITBI-E1 Homo sapiens genomic clone 2590621,
  EST 12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BG388094 651 bp mRNA linear EST 12-MAR-602413054F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4521732 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 AATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 TACATATAGGCTGGACGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG 247
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Pred. No. 5.2e-06;
0; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 633.
Location/Qualifiers
1. .651
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/clone="IMAGE:4521732"
/clone_lib="NIH_MGC_92"
                                                                              BG388094.1 GI:13281540
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70.8%;
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AA825901.1 GI:2899213
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72.6%;
                                                                                                                                                                                                                                                                                                                                                                                     82; Conservative
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Other_GSSs: CTTBI-EI-2590621.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
Fax: 301 838 0208
Email: hbe@tigr.corg
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.corg/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="sperm"
/note="Vector: pBeloBACI1; Site_1: EcoRI; Site_2: EcoRI;
Calrech Human BAC Library D"
109 c 113 g 145 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclic amplification and selection of target genes regulated by Pax3 and PAX3/FKHR in embryogenesis and alveolar rhabdomyosarcoma Unpublished (2000)
Contact: Friedman TB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Molecular Genetics
National Institute on Deafness and Other Communication Disorders,
National Institutes of Health
5 Research Court, Room 2A-15, Rockville, MD 20850, USA
Tel: 301 402 7580
Fax: 301 496 7882
Email: friedmanidGo.nih.gov
Plate: 02 row: e column: 08
Seg primer: -21M3 forward primer (ABI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 bp DNA linear GSS 01-MAR-ew02e08.x1 PAX3/FKHR CASTing Library 'ew' Homo sapiens genomic clone ew02e08 random, DNA sequence.
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Pred. No. 6.6e-06;
0; Mismatches 34;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                            /clone="2590G21"
/clone_lib="CITBI-E1"
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71.28;
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Matches 84; Conservat
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 726 Std Error: 0.00
Seq primar: -40m13 fwd. ET from Amersham
High quality sequence stop: 388.

Locatlon/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA825901 389 bp mRNA linear EST 09-JUN-1998 od52hll.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371621 3' similar to contains Alu repetitive element; contains element MER9 repetitive element; , mRNA sequence.
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Email: capabs.remail.ih.gov
Email: capabs.remail.ih.gov
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                     /note="Vector: pGEM-T Easy; Human genomic DNA was partially digested with Sau3AI, ligated to ds linkers, and enriched for binding to human PAX3/FKHR protein using a Whole Genome PCR-based strategy. DNA fragments containing putative PAX3/FKHR binding sites were amplified by PCR and cloned into pGEM-T Easy (Promega). The ligation products were transformed into DH10B electrocompetent cells (Life Technologies)."
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1 (Dases 1 to 389)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 ITTITATITAACCAATAATCITITGIATATTTATACCIGITAAAAATTCAGAAATGTCAA 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 303;
/clone="ew02e08"
/clone_lib="PAX3/FKHR CASTing Library 'ew'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63.4; DB 12;
Pred. No. 7.3e-06;
0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html
                                                                                                           /lab_host="DH10B"
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(Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHW, pregnant uterus NDHPU, and fetal heart NDHHI9W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization fraction. The dilver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 70 75 9 86 t
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439 bp DNA linear GSS 08-OCT-1998
HS_3203_A2_A05_MR CIT Approved Human Genomic Sperm Library D Homo
saplens genomic clone Plate=3203 Col=10 Row=A, DNA sequence.
AQ150673. GI:3544131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 43)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B" 95 g 114 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                        CTTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAAAAATTCAGAAATGTCA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62.8; DB 12; Length 439;
Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                               20.9%; Score 62.8; DB 9; Length 342; llarity 71.9%; Pred. No. 1e-05; Conservative 0; Mismatches 32; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
TEL: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3203 Col=10 Row=A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 439.
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Plate: 3203 row: A colu
Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                        Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                        Best Local Sim
Matches 82;
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                                  AI092525 342 bp mRNA linear EST 18-AUG-1998 qa38£07.x1 Soares_NhHMPu_S1 Homo sapiens CDNA clone IMAGE:1689061 3' similar to contains Alu repetitive element;, mRNA sequence. AI092525
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index.

Unpulished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infedimage.llnl.gov) for further information.

Seq primer: -40ml3 fwd. ET from Amersham.
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/clone="IMAGE:1689061"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 TTCAAATGACTACCCAAATGAGTTTTATAAAACTGATCAAAAAATTTAAAAATTCCAAGCCGG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 TIAATITCTTTTCTCCAIGCATAIGGCTCAAAGGGAAGIGTCTAIGGCCCTIGCTTTTA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 TTAGTGAGTTTTATTCAGACCAAGTGGTGAAATCTGAAAATTGAGATTTCACATGTATGA 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 GCACGGIGGCICACCCCIGIAAICCCAGCACTITGGGAGGCCGAGGC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.9%; Score 63; DB 9; 18est Local Similarity 61.1%; Pred. No. 9.3e-06; Matches 102; Conservative 0; Mismatches 65
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                           /organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Trissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Trissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-CAPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llh.gov/bbrp/Aimage/Aimage.html
Insert Length: 966 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 280
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281 bp mRNA linear EST 13-MAY-1999 tq49g04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2212182 3/ similar to contains Alu repetitive element; contains L1.t1 L1 repetitive element; , mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 281)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                        303 AGAGCIGAGGAICTAAAGATITITACTITGAITTAICCCATTAICAICTGCAGGGAAACA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 ATAATCTTTTGTATTTATACCTGTTAAAATTCAGAAATGTCAAGGCCGGGCACGGTG 262
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                                                                                                                       AAAGGGAAGTGTCTATGGCCCTTGCTTTTATTTAACCAATAATCTTTTGTATATAA
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/db_xref="taxon:9606"
/clone="IMAGE:2212182"
/clone=lib="NOI_CGAP_Utl"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH108"
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Pred. No. 1.5e-05;
0; Mismatches 23; Indels
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76.8%;
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Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7880
Fax: 617 738 6996
Email: ccmorton@bics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
http://www.nisc.nih.gov).
This clone is available royalty-free through LIML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLAM6178 row: I column: 16
Seq primer: MI3RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R. and Morton, C.C. Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening genomics 23, 42-50 (1994)
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Homo sapiens cDNA clone
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                                                              373 TACTTATCTCNTATGTAGGTAGGTGCTTTCTTCCTCTGATTATTTTAAGAATTTACTT 314
                                                                                                                       182 CCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTTATACCTGTTAAAAATTCAGAA 241
                                       ACAAGTCATGGGTTTAATTTCTTTTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATGG 181
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                                                                                                                                                                                                                       313 TTACCTGGCCTGGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGG 255
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 1e-05;
0; Mismatches 47; Indels
73; Indels
0; Mismatches
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AW020486.2 GI:15330169
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ENKATYOGE, METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 400)

1 (bases 1 to 400)

1 (bases 1 to 400)

2 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

7 Washington university Project

7 Unpublished (1995)

7 Contact: Wilson RK

7 Washington university School of Medicine

7 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

7 Fel: 314 286 1800

7 Fest: 11 24 286 1800
                           A00 bp mRNA linear EST 24-AUG-1995 yg02fil.sl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:195789 3' similar to contains Alu repetitive element; contains R89296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: estewatson.wustl.edu
Insert Size: 1115
High quality sequence stops: 268
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1115, Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 ACATACATTGAGATATTATTCAGCCTTAAAAAAGAAGAAAAATCATGGCCGGGCGCGGTG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 GCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGAGGC 301
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Location/Qualifiers
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/note="Organ: marrow, Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES POR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-WT0160-
281100-021-g01&t3=2000-11-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 310.
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                                                                    310 bp mRNA linear EST 18-JAN-2001
RC1-MT0160-281100-021-g01 MT0160 Homo sapiens cDNA, mRNA sequence.
BF8988122.
BF898122.1 GI:12289581
EST.
                                                                                                                                                                                                                                      Homo sapiens

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 310)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., Gollvelra,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                    \operatorname{Simpson}, A . \mathbf{J} Shotgun sequencing of the human transcriptome with ORF expressed shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 AAGTGTCTATGGCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATTTTATACCTGTT 229
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164 GCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGAC 202
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/db_xref="taxon:9606"
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1 Similarity 67.2%;
88; Conservative
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Fax: +55-11-2707001
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 408)

1 (bases 1 to 408)

1 (bases 1 to 408)

Chissoe, S., Dietrich, N., Bubque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Le, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
H71349
408 bp mRNA linear EST 26-OCT-1995
yu55h06.s1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone
IMAGE:230075 3' similar to contains Alu repetitive element; contains
H71349.1 GI:1043165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington university School of Medicine
4444 Forest park Parkway, Box 8501, St. Louis, MO 63108
7444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Email: est@watson.wustl.edu
Insert 51z=1145
Insert 51z=1145
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium, alidolange.llnl.gov) for further information.
Insert Length: 1145
Seq primer: Promega -21m13
High quality Sequence stop: 213.
High quality Sequence stop: 213.
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Matches 76; Conservative
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Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ds.
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Hereditary hæmoch
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This genomic DNA sequence corresponds to the human gene whose mutated form is associated with hereditary haemochromatosis (HH).

To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HLA region of chromosome 6. A physical clone coverage was then generated extending from D65265, which is a marker that is centromeric of HLA-A in a telomeric direction through D65276, a marker at which the allelic association was no longer observed. A single mutation of seasons.

C (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 66% of affected chromosomes and in 4% of unaffected chromosomes.

C I results in a Cys to Tyr substitution in the encoded protein (see AAW36499) at a critical disulphide bridge important for secondary structure. The following are claimed: the HH genomic DNA (1), a critical disulphide bridge important for secondary structure. The following or expression vector, host cells; a peptide product chosen from the HH gene product, its variants contained: a cloning or expression vector, is variants are allouded for absence of the common HH gene mutation; an animal model for the HH disease; metal chelation contained the mitigation of injury due to oxidative process in vivo or mitigation of inno verload, a method for screening potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hereditary haemochromatosis gene and variants – useful for diagnosis and treatment of hereditary haemochromatosis disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antisense oligonucleotide directed against a transcriptional product of a nucleic acid sequence as above; and oligonucleotides for pairs of oligonucleotides covering a range of nucleotides from (I). (Ia) or their variants, useful for detecting a polymorphism in the HH gene. The invention also relates to methods for screening diagnosis, prenatel screening and diagnosis, and theraples of HH disease, including gene therapy, protein and antibody-based therapeutics, and small molecule
                                                                                                                                                                                               if to A substitution (24d1 mutation associated with HH), results in Cys to Tyr substitution"
                                                    g "C to G substitution (24d2 mutation) results in His to Asp substitution"
                                                                                                                                           "A to T substitution (24d7 variant) results in Ser to Cys substitution'
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Fsuchihashi Z, Wolff RK;
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                                               100.0%; Score 301; DB 18; Length 10825; 100.0%; Pred. No. 1e-79; 0; Indels 0; Mismatches 0; Indels 0;
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           Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;
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Matches 301; Conservative
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products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                                                                         100.0%; Score 301; DB 22; 100.0%; Pred. No. 1e-79;
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P-PSDB; AAB36870.
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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-call differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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Pred. No. 1e-79;
Mismatches 0;
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Disclosure; Fig 3; 108pp; English
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                      Thomas WJ, Drayna DT,
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                                                                                                                                                                                                                                                                                                            61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
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                                                                                                                                                                                                                                                               1 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGTCCCTCTCCCAAATTC 60
                                                                                                                                                                                                                                          Gaps
                                   New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                  tch 100.0%; Score 301; DB 22; Length 10825; al Similarity 100.0%; Pred. No. 1e-79; 301; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                   Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human hereditary hemochromatosis 24d1/2 mutation DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds.
                                                                                 Disclosure; Fig 3; 108pp; English.
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96US-0632673.
96US-0652265.
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   WPI; 2001-006341/01
               P-PSDB; AAB36871
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23-MAY-1996;
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products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wolff RK;
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                                                                                                                                          New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                    present invention relates to hereditary hemochromatosis gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA of a histocompatibility iron loading (HFE) gene.
Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 10825 BP; 2999 A; 2252 C; 2648 G; 2926 T; 0 other;
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Pred. No. 1e-79;
  Gnirke A, Ruddy D,
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Best Local Similarity 100.0%;
Matches 301; Conservative 0;
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Gaps

; 0

Length 12146; Indels 5639

300

us-09-497-957-3_4570-4870.rng

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabletic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                               5520 tgggaagggactttctcaatcctagagtctctaccttataattgagatgtatgagacagc 5579
                                                                                                                                                                                                                                                         TGGGAAGGGACTITCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
                                                  1 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTCTCCAAATTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human musculoskeletal system related polynucleotide SEQ ID NO 3112.
                                                                                                                                             121 CACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATG
                                                                                                                                                                     5580 cacaagtcatgggtttaatttcttttctccatgcatatggctcaaagggaagtgtctatg
                                                                                                                                                                                                         AATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGAGG
                                                                                                                                                                                             GCCCTTGCTTTTTATTTTAACCAATAATCTTTTGTATATTTATACCTGTTAAAATTCAGA
   100.0%; Score 301; DB 21;
100.0%; Pred. No. 1.1e-79;
iive 0; Mismatches 0;
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2000US-0184664.
2000US-0186350.
2000US-0189874.
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2000US-0198123.
2000US-0205515.
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2000US-0215135.
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2000US-0217487.
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2000US-0220964.
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                           Conservative
               Local Similarity
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16-MAR-2000;
18-MAR-2000;
18-APR-2000;
19-MAY-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
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                          301;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic
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26-JUL-2000; 14-AUG-2000;

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08-NOV-2000; 2000US-0246525.
08-NOV-2000; 2000US-0246525.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246532.
08-NOV-2000; 2000US-0246532.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0249201.
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20000S-0251856.
20000S-0251868.
20000S-0251869.
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(HUMA-) HUMAN GENOME SCI INC

SM Rosen CA, Barash SC, Ruben

WPI; 2001-451937/48

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis -

Example 2; SEQ ID NO 3112; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; ss.
parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                            CACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATG 180
                                                                                                                                                                                                                             690 cacaagtcatgggtttaatttcttctccatgcatatggctcaaagggaagtgtctatg 749
                                                                                                                                                                                                                                                             241 AATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGAGG 300
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                                                                                                                                               TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
                                                                                                                                                                                                                                                   GCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAAAAATTCAGA 240
                                                                                                                          1 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTCTCCAAATTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hereditary haemochromatosis subregion from an HH affected individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hereditary haemochromatosis gene products - used to develop products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for the diagnosis and treatment of hereditary disorders in iron metabolism
                                                                                    DB 22; Length 5749;
                                                   Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;
                                                                                Query Match 99.5%; Score 299.4; DB 22; Length Best Local Similarity 99.7%; Pred. No. 2.5e-79; Matches 300; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomas WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruddy DA,
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                                                                                                                                                                                                                                                                                                                                                                                                            AAV57903 standard; DNA; 237326 BP.
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Tsuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROG-) PROGENTIOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-240014/21.
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products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis subregion from an hereditary haemochromatosis subregion from an hereditary haemochromatosis (HH) affected individual. Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (HF), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a RoRet gene which are homologues of a type 1 sodium transport gene, and can can be used to homelogues of a type 1 sodium transport gene, and can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; diagnosis; colon cancer; cancer; malignant; chromosome mapping; detection; colon cancer cell line Kml2L4-A; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.9%; Score 294.6; DB 19; Length 237326; 98.7%; Pred. No. 2.7e-77; ive 0; Mismatches 4; Indels 0; G
                                                                               present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarly be used for hypophosphatemia.
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Claim 1; Fig 9; 209pp; English.
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Best Local Similarity 98.79
Matches 297; Conservative
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WO200157182-A2.
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27-SEP-2000;
The present invention describes a library of polynuclectides comprising 1079 nuclectide sequences (given in AAH30067 to AAH3115). Also described are: (1) an isolated polynuclectide (I) having at least 90% identity to one of the 1079 sequences; (2) a recombinant host cell containing (1); (3) an isolated polypeptide (II) encoded by (I); (4) an antibody that specifically binds to (II); (5) a vector comprising (I); and (6) a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell comprising detecting a gene product encoded by 65 fthe 1079 sequences given in the specification. The polyvacientides are used to monitor patients having for susceptible) to cancer to detect potentially malignant events at a molecular level before they are of entectable at a gross morphological level. The polyvacientides are also useful for monitoring the efficacy of various therapies and preventive interventions. Polynuclectide probes based on the disclosed sequences are useful for chromosome mapping and detection of transcription levels. The 1079 polynuclectide sequences were derived from a human colon cancer cell line Km12L4-A cDNA library.
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                                                                                                                                                                                     PD, Sudduth-Klinger J;
C, Pot D, Kassam A;
n M, Drmanac S, Labat I;
Stache-Crain B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                              Polynucleotide library comprising 1079 defined sequences, useful in the form of an array to detect cancer or susceptibility to cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 429 BP; 142 A; 75 C; 75 G; 113 T; 24 other;
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Glese K, Randazzo F, Kennedy GC, PP,
nanac R, Cikvenjakov R, Dickson M,
Kita D, Garcia V, Jones LW, Staci
                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 229-230; 502pp; English.
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                                                           98US-0102180.
98US-0102380.
98US-0103815.
98US-0105877.
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                                                                                                                                                                      Williams LT, Escopeuc Feinhard C, Giese K, F
                                                                                                                                                                                                                                 Leshkowitz D, Kita D,
                                                                                                                                       (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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Best Local Similarity
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18-APR-2000;
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(HUMA-) HUMAN GENOME SCI INC.
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2000US-0246475.
2000US-0246476.
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17-NOV-2000;
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17-NOV-2000;
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01-DEC-2000;
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Barash SC, Ruben SM;

Rosen CA,

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) anno acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polyuucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the unclaic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially to AAK87694 represent human immune/haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK49421 to AAK84950 and AAM82169 represent sequences used in the exemplification of the present invention.
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                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                          Disclosure; SEQ ID NO 19848; 3071pp + Sequence Listing; English.
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Pred. No. 5.3e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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72.1%;
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2000US-0184664.
2000US-0186350.
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                                                                      useful for preventing,
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Best Local Similarity
               WPI; 2001-483426/52.
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2000US-0234999
2000US-0235484
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200US-0236369
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2000US-0215135.
2000US-021647.
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2000US-0220963.
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2000US-0225447.
2000US-0225757.
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2000US-0226279.
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2000US-0229513.
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(HUMA-) HUMAN GENOME SCI INC.
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200005-0251868
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200005-0251989
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11-DEC-2000; 2000US-0254097
05-JAN-2001; 2001US-0259678
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20-0CT-2000; 20-0C
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SM; Ruben Barash SC, CA, Rosen

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

Disclosure; SEQ ID NO 33338; 3071pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased

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20000S-022950
20000S-0230438
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20000S-0231241
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20000S-0231414
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25-SEP-2000; 2
25-SEP-2000; 2
26-SEP-2000; 2
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02-0CT-2000; 2
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02-0CT-2000; 2
13-0CT-2000; 2
13-0CT-2000; 2
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expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 sequences from the present invention. AAK64942 to AAK54950 and AAX82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 TITTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAAAAATTCAGAAATGTCAAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                       Query Match 20.4%; Score 61.4; DB 22; Length 26110; Best Local Similarity 72.1%; Pred. No. 5.3e-08; Matches 80; Conservative 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 GCCGGGCACGCIGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGAGG 300
                                                                                                                                                                                                                                                                                            Sequence 26110 BP; 7464 A; 4942 C; 5567 G; 8137 T; 0 other;
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20000S-0216890.
20000S-0217487.
20000S-0217496.
20000S-0218290.
20000S-0220963.
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2000US-0214886.
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2000US-0186350.
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2000US-0225267
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17-MAR-2000;
18-APR-2000;
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07-JUN-2000;
28-JUN-2000;
07-JUL-2000;
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11-JUL-2000;
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Length 584; Indels 20.3%; Score 61; DB 22; 56.9%; Pred. No. 1.7e-08; ive 0; Mismatches 85

Matches 112; Conservative

Local Similarity

Query Match

165 AAGGGAAGTGTCTATGGCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTTATAC 224 155 agataaacaaaggaggaaagattcatgtaagaaaatgccatgcaactacaaaatgggata

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225 CTGTTAAAAATTCAGAAATGTCAAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCA

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) supplement the patients own production of (I). Additionally, (I) proteins and polynucleotides may be used to protein content manune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic concer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent invention.
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08-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 208-NOV-2000; 217-NOV-2000; 217
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Human; reproductive system related antigen; reproductive system disorder;

gene therapy;

cancer;

Human reproductive system related antigen DNA SEQ ID NO: 5454.

21-NOV-2001 (first entry)

AAL02766;

AAL02766 standard; DNA; 6534 BP.

AAL02766

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2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0214886.
                                                                                                                                2000US-0189874.
2000US-0190076.
                                                                                                                                                                         2000US-0216647.
2000US-0216880.
                                                                                             17-JAN-2001; 2001WO-US01339
                                                                                                                                                                                           2000US-0217496
                                                                                                                                                                                                             2000US-0220964
                                                                                                                                                                                     2000US-0217487
                                                                                                                                                                                                                                                                                         2000US-0226279
                                                                     WO200155320-A2.
                                                                                                                                                                        07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
26-JUL-2000;
                                                                                                                                16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                       07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
                                                          Homo sapiens.
                                                                                                                                                                                                                  14-AUG-2000;
                                                                                                                                                                                                                              14-AUG-2000;
14-AUG-2000;
                                                                                                                          02-MAR-2000;
                                                                                                                                                                                                                                                      14-AUG-2000;
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                                                                                 02-AUG-2001
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Sequence 584 BP; 196 A; 109 C; 135 G; 144 T; 0 other;

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PR 22-AuG-2000; 20000S-0226681.
PR 22-AuG-2000; 20000S-0225668.
PR 22-AuG-2000; 20000S-0227182.
PR 30-AuG-2000; 20000S-022943.
PR 10-SEP-2000; 20000S-022943.
PR 01-SEP-2000; 20000S-022944.
PR 01-SEP-2000; 20000S-022944.
PR 05-SEP-2000; 20000S-022944.
PR 06-SEP-2000; 20000S-022944.
PR 06-SEP-2000; 20000S-023944.
PR 06-SEP-2000; 20000S-023944.
PR 06-SEP-2000; 20000S-023944.
PR 06-SEP-2000; 20000S-023144.
PR 06-SEP-2000; 20000S-023144.
PR 06-SEP-2000; 20000S-023144.
PR 06-SEP-2000; 20000S-023198.
PR 14-SEP-2000; 20000S-023198.
PR 25-SEP-2000; 20000S-023198.
PR 26-SEP-2000; 20000S-02319
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1861 aaattatttagtggctacttgtggttgtagagtaaggtccaaattccaaagcctttaaaa 2920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 TAACCAATAATCTTTTGTATATTTATACCTGTTAAAATTCAGAAATGTCAAGGCCGGGC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 AATTICITITCCCCATGCATATGGCTCAAAGGGAAGTGTCTATGGCCCTTGCTTTTATT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 5454; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.3%; Score 61; DB 22;
60.6%; Pred. No. 4.1e-08;
tive 0; Mismatches 65;
                  17-NOV-2000; 200005-0249208.
17-NOV-2000; 200005-0249209.
17-NOV-2000; 200005-0249211.
17-NOV-2000; 200005-0249211.
17-NOV-2000; 200005-0249211.
17-NOV-2000; 200005-0249211.
17-NOV-2000; 200005-0249213.
17-NOV-2000; 200005-0249215.
17-NOV-2000; 200005-0249216.
17-NOV-2000; 200005-0249216.
17-NOV-2000; 200005-0249216.
17-NOV-2000; 200005-0249244.
17-NOV-2000; 200005-0249244.
17-NOV-2000; 200005-0249244.
17-NOV-2000; 200005-0249244.
17-NOV-2000; 200005-0249265.
17-NOV-2000; 200005-0249290.
17-NOV-2000; 200005-0249290.
17-NOV-2000; 200005-0249290.
17-NOV-2000; 200005-0249290.
17-NOV-2000; 200005-0249290.
17-NOV-2000; 200005-0251989.
05-DEC-2000; 200005-0251479.
06-DEC-2000; 200005-0251479.
06-DEC-2000; 200005-0251479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 60.6 Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein of the invention
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PPR R R R PPR R R R PPR R R PPR PP
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RESULT 14 AAC27863 · ID AAC27863 standard; cDNA; 344 BP.

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; hamanopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 6555; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3242 BP; 949 A; 656 C; 666 G; 971 T; 0 other;
                                                                                                                                                                                                      26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                        28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                            HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AA006564
                                                                                                                                 WO200164835-A2.
                                                                                                                                                                  07-SEP-2001
                                                                                                                                                                                                                                                                                                                                Tang YT,
         δλ
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0
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                                                                                                                             sequence tag; secreted protein; cDNA isolation;
mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 TGCTTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAAAATTCAGAAATGT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 344 BP; 96 A; 79 C; 83 G; 85 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                      Human secreted protein 5' EST, SEQ ID NO: 31938.
                                                                                                                                                                                                                                                                                                                                                                                              Glordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 60.6; DB 21
Pred. No. 1.8e-08;
0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 31938; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                              Duclert A,
                                                                                                                                        gene therapy; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.1%;
Best Local Similarity 70.4%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                      99US-0122487
                                                    (first entry)
                                                                                                                           expressed
                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-500381/45.
                                                                                                                       EST;
                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                             EP1033401-A2
                                                                                                                                                                                                                                                                                   21-FEB-2000;
                                                                                                                                                                                                                                                                                                                      26-FEB-1999;
                                                  06-OCT-2000
                                                                                                                                                                                                                                                 06-SEP-2000
                                                                                                                         Human; 5'
                AAC27863;
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Liu C,

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ö
                                                                                         211 TIGIAIATITATACCIGITAAAAATTCAGAAATGTCAAGGCCGGGCACGGTGGCTCACCC 270
                                        Gaps
                                     ó;
20.1%; Score 60.6; DB 22; Length 3242; 79.1%; Pred. No. 4.2e-08; 1ve 0; Mismatches 19; Indels 0;
                                                                                                                                       271 CTGTAATCCCAGCACTTTGGGAGGCCGAGGC 301
                                                                                                                                                               CTGTAATCCCAGCACTTTGGGAGGCCGAGGC
                  Similarity 79.1%; 72; Conservative
                Best Local Similarity
Matches 72; Conserv
 Query Match
                                                                                                       328
                                                                                                                                                                            268
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Search completed: June 19, 2002, 11:01:22 Job time: 7640 sec

Human polynucleotide SEQ ID NO 6555

(first entry)

06-NOV-2001

AAI86495;

RESULT 19
AA186495/C
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AC AA186
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DT 06-NC
XX

AAI86495 standard; cDNA; 3242

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Appli Appli

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Run on:

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sequence 3, 18 Sequence 35, 18 Sequence 37, 18 Sequence 17, 18 Sequence 117, 18 Sequence 117, 18 Sequence 17, 
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David,
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TTLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SCUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATIOS SISTEMS: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTONNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
US-09-385-982-32
US-08-870-126-7
US-09-630-706-10
US-09-630-706-10
US-09-128-155-15
US-09-347-114A-81
US-09-347-114A-80
US-09-367-384-7
US-09-305-384-7
US-09-305-384-1
US-09-305-384-1
US-09-305-384-1
US-09-305-384-1
US-08-466-974-1
US-08-466-974-1
US-08-466-974-1
US-08-466-974-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08652265 Patent No. 6025130 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Thomas, Winston J. APPLICANT: Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-503-444A-7
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length: 2000000000
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Result

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/note= "No. 6025130mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
allele"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTTATACCTGTTAAAAATTCAGA
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LOCATION: 3852..3891
OTHER INFORMATION: force- start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C) OTHER INFORMATION: allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                      /note- "start and stop positions for normal or wild-type (unaffected) genomic sequence surrounding variant for 24d1(G) allele (SEQ ID NO:20)"
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                                                                                                             UCCATION: 140.,7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: CDNA (SEQ ID NO:9)"
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NAMEKEY: allele
LOCATION: replace(1872, "c")
LOCHEN INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
.... THEORMATION: /label= 24d2
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100.0%; Score 301; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.6e-86;
Matches 301; Conservative 0; Mismatches 0;
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NAME/KEY: allele
LOCATION: replace(3878, "a")
OTHER INFORMATION: (unaffected)
OTHER INFORMATION: (label= 24d)
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OTHER INFORMATION: /label= 24
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis
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/note= "Hereditary Hemochromatosis (HH)
gene 24d1 allele"
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                                                              GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Henchromatosis Gene
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY. San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17957-000500
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111.3834
COMPUTER READABLE FORM:
CMPUTER: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                        Sequence 3, Application US/08652265
Patent No. 6025130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 175
TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
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STRANDEDNESS: sing]
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION:
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NAME/KEY:
LOCATION:
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US-08-652-265-3
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                     0;
                                                                                                            Length 10825;
/phenotype= "Hereditary Hemochromatosis
                                                                                                                                                Indels
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APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Grirke, Andreas
APPLICANT: Grirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
ITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CCOUNTRY: USA
ZIP: 9411-3834
COMPTTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: DATE COMPALIBLE
COMPUTER: PATENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING APPLICATION:
FILING APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                            100.0%; Score 301; DB 3;
100.0%; Pred. No. 6.6e-86;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELERAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
                                      /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08652265 Patent No. 6025130
                                                                                                                               Best Local Similarity 100. Matches 301; Conservative
) OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-652-265-3
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US-08-652-265-5
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4690 CACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATG 4749
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  4630 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGAGAG
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: -
COATION: 5507..6023
COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant other INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: -
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                       LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
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; Sequence 7, Application US/08652265
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: replace
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4630 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACTTATAATTGAGATGTATGAGACAGC 4689
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                                                                                                                                                                                                                                                                                                   Length 10825;
  /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                /phenotype- "Hereditary Hemochromatosis
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APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Roddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 301; DB 3; Best Local Similarity 100.0%; Pred. No. 6.6e-86; Matches 301; Conservative 0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
ODERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
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1155 Avenue of the Americas
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FILING DATE: 04-APR-1997
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APPLICATION NUMBER: US 08/652,265
               CTHER INFORMATION: /label= 24d2
CTHER INFORMATION: /label= 24d2
FEATURE:
NAME/KEY: allele
LOCATION: replace(5834, "a")
CTHER INFORMATION: /phenotype=
CTHER INFORMATION: /label= 24d1
US-08-652-265-7
                                                 /label= 24d2
                                                                                                                                                                                                  /label= 24d1
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CURRENT APPLICATION DATA:
OTHER INFORMATION:
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ZIP: 10036-2811
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STATE:
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OTHER INFORMATION: /Product= "Hereditary Hemochromatosis OTHER INFORMATION: and 24d2 mutations"

OTHER INFORMATION: Onote= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: Gene containing a combination of both OTHER INFORMATION: 24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and 24d2 mutations"
/note= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: cDNA containing a combination of both OTHER INFORMATION: 24d1 and 24d2 alleles
OTHER INFORMATION: (SEQ ID NO:12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)".
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LOCATION: 5507..6023
OTHER INFORMATION: /note= start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
                            APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                      E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY-AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
FEGGESTRATION NUMBER: 17957-000500
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELERAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTEREISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: replace(3872, "g")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                   STREET: TWO DANCE.
CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 140..73:
OTHER INFORMATION:
OTHER INFORMATION:
             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                      ADDRESSEE:
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4870 C 4870
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US-08-834-497A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 C 301
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Hereditary Hemochromatosis (HH) gene
allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: .
LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d1(G) OTHER INFORMATION: allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(3.153, 7107..7147)
COTHER INFORMATION: /product= "No. 6140305mal or wild-type (unaf OTHER INFORMATION: Hereditary Hemochromatosis OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCHER INFORMATION: Anote-"start and stop positions for OCHER INFORMATION: Anote-"start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 2442(C) OTHER INFORMATION: allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: cDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /phenotype= "normal or wild-type (unaffected)"
/label= 2461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: replace(3872, "c")
OTHER INPORMATION: 'phenotype= "normal or wild-type
OTHER INPORMATION: (unaffected)"
OTHER INPORMATION: /label= 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: replace(3878, "a")
OTHER INPORMATION: /phencype="normal or wild-type
OTHER INPORMATION: /label=2467
OTHER INPORMATION: /label=2467
                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 24,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
TELEX: 6641 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STARNEDNESS: SINGle
               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: /phenotype=

CTHER INFORMATION: /phenotype=

CTHER INFORMATION: (unaffected)"

CTHER INFORMATION: /label= '1'.
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23-MAY-1996
N: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                 241 AATGICAAGGCCGGGCACGGIGGCICACCCCIGIAAICCCAGCACTIIGGGAGGCCGAGG 300
                                                                                                                                                                                                     61 TGGGAAGGGACTTICTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
                                                                                                                                                                                                                                                                                                            121 CACAAGTCATGGGTTTAATTTCTTTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATG 180
                                                      Gaps
                                                                                                    1 GGCACGGAATCCCTGGTTGGAGTTCAGAGGTGGCTGAGGCTGTGTGTCCTCTCCAAATTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                181 GCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAAAAATTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
Length 10825;
                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: FLORPY disk
COMPUTER: FLORPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COURRENT SYSTEM: Windows 95
SOFTWARE: FASTESO for Windows Version 2.0b
SOFTWARE: VAPPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: US/08/834,497A
FILING DATE: 134
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY'1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION 1514
CLASSIFICATION 1514
PRIOR PAPELICATION 1514
PRIOR PAPELICATION 1514
CLASSIFICATION 1514
PRIOR PAPELICATION 1514
PAPELICATION 1514
100.0%; Score 301; DB 3; ilarity 100.0%; Pred. No. 6.6e-86; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08834497A Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1155 Ave
CITY: New York
STATE: New York
  Query Match
Best Local Similarity
Matches 301; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation"

OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: gene 24d2 allele"
                                                                                                                                                                                                                  GENERAL INCRMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Reder, John N.
APPLICANT: Ruddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARRE: FastSEQ for Windows Version 2.0b
SOFTWARRE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-ARR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: S14
ATTORNEY AGENT INFORMATION:
NAME: POISSANT, BIAN M.
REGISTRATION NUMBER: 8907-0056-999
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-4935
TELEPKA: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base Pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                 Sequence 5, Application US/08834497A
Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10036-2811
                                                                            4870 C 4870
                                                                                                                                                           US-08-834-497A-5
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                                   301 C 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAAAAATTCAGA 240
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                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS

LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product- "Hereditary Hemochromatosis OTHER INFORMATION: mutation"

OTHER INFORMATION: /nocte- "Hereditary Hemochromatosis (HH) OTHER INFORMATION: gene 24d1 allele"

NAME/KEY:
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100.0%; Score 301; DB 3; Length 10825;
Best Local Similarity 100.0%; Pred. No. 6.6e-86;
Matches 301; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: replace(5834, "a")
OTHER INFORMATION: /Phenotype- "Hereditary Hemochromatosis
OTHER INFORMATION: /label- 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "start and stop positions for
genomic sequence surrounding variant
for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: -
LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 550-4935
                                                                                                                      TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: -
LOCATION: 5507..6023
OTHER INFORMATION: /r
OTHER INFORMATION: ge
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NAME/KEY: allele
LOCATION: replace
                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4750 GCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAAAAATTCAGA 4809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4570 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCTGCTCTCCCAAATTC 4629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAAAAATTCAGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGTCCCTCTCCCAAATTC 60
                                                                                                                                                                                                                                                                                                                                                                                      , LUCATION: replace(3872, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
; OTHER INFORMATION: /label= 24d2
US-08-834-4978-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 301; DB 3; Length 10825; Best Local Similarity 100.0%; Pred. No. 6.6e-86; Matches 301; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS NUMBER OF SEQUENCES: 76 CORRESPONDENCE ADDRESS:
                                                                                                                        LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
NAME/RET: LOCATION: 5507..6023
COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"
LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08834497A Patent No. 6140305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
                                                                                                          3852..3891
                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: allele
LOCATION: replace
                                                                                'EATURE:
NAME/KEY:
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NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: replace(3872, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and 24d2 mutations"
/note= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "start and stop positions for coDNA containing a combination of both 24d1 and 24d2 alleles (SEQ ID NO:12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "start and stop positions for genomic sequence surrounding variant for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 3852..3891

OTHER INFORMATION: /note= "start and stop positions for

OTHER INFORMATION: genomic sequence surrounding variant

OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: FILPPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows 95
OSTEWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMINICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                          CURKENT APPLICATION DATE:

APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/652,265
FILING DATE: 33-MAY-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION 14
PRIOR APPLICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: 507..6023
LOCATION: 5507..6023
OTHER INFORMATION: 700
OTHER INFORMATION: GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 140..7319
OTHER INFORMATION: CD
OTHER INFORMATION: CD
OTHER INFORMATION: CS
OTHER INFORMATION: C5
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OTHER INFORMATION:
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NAME/KEY:
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TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
16-Apr-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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LOCATION: 140..7319
OTHER INFORMATION: /
OTHER INFORMATION: n
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OTHER INFORMATION:
OTHER INFORMATION:
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FEATURE:
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NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 301; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-503-444A-1
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                                                                                                                                                                                                                                                                                                                                                                                                      121 CACAAGTCATGGGTTTAATTTCTTTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATG 180
                                                                                                                                                                                                                                                                                                         61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATTTTATACCTGTTAAAAATTCAGA 240
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                   1 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTCTCCAAATTC 60
                                                                                                                                                                                                  ó;
                                                                                                                                                             Length 10825;
                                            /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09503444A

Patent No. 6228594

GENERAL INFORMATION

APPLICANT: Thomas, Winston J.

APPLICANT: Feder, John N.

APPLICANT: Ruddy, David

APPLICANT: Ruddy, David

APPLICANT: Tsuchinashi, Zenta

APPLICANT: Tsuchinashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA
                                                                                                                                                           Query Match
100.0%; Score 301; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.6e-86;
Matches 301; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/503,444A FILING DATE: 14-Feb-2000 CLASSIFICATION:
       NAME/KEY: allele
LOCATION: replace(5834, "a")
COTHER INFORMATION: /phenotype= 'OTHER INFORMATION: /label= 24d1
US-08-834-497A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PRILING DATE: 23-May-1996
PRIOR APPLICATION DATE: 28-May-1996
APPLICATION NUMBER: 08/632,673
                                                                                                                                                         Query Match
Best Local Similarity
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Hereditary Hemochromatosis (HH) gene
allele"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: G040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
OTHER INFORMATION: /note= "No. 6228594mal or wild-type (unaf
OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene
OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: -
LOCATION: 3852..3891
OCHER INFORMATION: / foote= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C) OTHER INFORMATION: allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "start and stop positions for
normal or wild-type (unaffected) genomic
sequence surrounding variant for 24d1(G)
allele (SEQ ID NO:20)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "start and stop positions for normal or wild-type (unaffected) allele CDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: allele
LOCATION: replace(3872, "c")
CHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: replace(3878, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 2447
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OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 301; DB 4;
100.0%; Pred. No. 6.6e-86;
11ve 0; Mismatches 0;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
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              4570 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCTGTGCCTCTCCAAATTC 4629
                                                                                                                                                              121 CACAAGTCATGGGTTTAATTTCTTTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATG 180
                                                                                         181 GCCCTTGCTTTTTATTTAACCAATAATCTTTTGTATATTTTATACCTGTTAAAATTCAGA
                                                                                                                                                                                                                                   4810 AATGTCAAGGCCGGGCACGGTCACCCTGTAATCCCAGCACTTTGGGAGGCCGAGG
                                                                                                                                                                                                                                                                                      241 AATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGAGG
1 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTCTCCAAATTC
                                                                     61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/503,444A FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION NUMBER: 08/632,673
FILING DATE: 16-APPL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-APPL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09503444A Patent No. 6228594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Poissant, Brian M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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4570 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCTCTCCCAAATTC 4629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4810 AATGTCAAGGCCGGGCACGGGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGGGG 4869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTTATCTTATAATTGAGATGTATGAGACAGC 120
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                                                                                                                                                                LOCATION: Join (361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product="Hereditary Hemochromatosis OTHER INFORMATION: mutation"
OTHER INFORMATION: /note="Hereditary Hemochromatosis OTHER INFORMATION: gene 24d1 allele"
NAME/KEY: -LOCATION: 140..7319
CAPTION: 140..7319
OTHER INFORMATION: /note="start and stop positions for OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: replace(5834, "a")
COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24dl
US-09-503-444A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 10825;
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LOCATION: 3852..3891
LOCATION: 3852..3891
COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant office allele (SEQ ID NO:41)"
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genomic sequence surrounding variant
for 24d1(A) allele (SEQ ID NO:21)"
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100.0%; Pred. No. 6.6e-86;
tive 0; Mismatches 0;
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                                                                                             MOLECULE TYPE: DNA (genomic)
LENGTH: 10825 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 301; Conservative
                                              STRANDEDNESS: single
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                                                                             linear
                                                                                                                                                   CDS
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NAME/KEY:
LOCATION:
                                                                           TOPOLOGY:
                                                                                                                                                   NAME/KEY:
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US-09-503-444A-5
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; Sequence 7, Application US/09503444A; Patent No. 6228594
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 301; Conservative
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PRIOR APPLICATION DATA:
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US-09-503-444A-7
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: foin(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: mutation"
OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH)
OTHER INFORMATION: gene 24d2 allele"
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LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)" FEATURE:
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OTHER INFORMATION: /note- "start and stop positions for OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                   APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PULDA STETLING
PURDA STETLING
APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATORNEY/AGENT INFORMATION:
NAME: POISSAIL, BIAD M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 38,462
REFERENCE/DOCKET NUMBER: 38,462
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-790-9090
TELECHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 21z-c..
TELEFAX: 61d.1
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 10825 base pairs "VPE: nucleic acid "VPE: nucleic acid "VPE: single
                Thomas, Winston J.
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                             New York
: USA
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        New York
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;
LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"
FEATURE: NAME/KEY: allele LOCATION: replace(3872, "g")
COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label- 24d2
                                                                                                                                                                                                                                                                                                                                                          Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INTENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 301; DB 4;
100.0%; Pred. No. 6.6e-86;
ive 0; Mismatches 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
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NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: Aproduct="Hereditary Hemochromatosis of THER INFORMATION: and 24d2 mutations"
OTHER INFORMATION: Anote="Hereditary Hemochromatosis (HH) OTHER INFORMATION: gene containing a combination of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: replace(5834, "a")
UTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: replace(3872, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 24d2
OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and 24d2 mutations" //note="Hereditary Hemochromatosis (HH) gene containing a combination of both 24d1 and 24d2 alleles"
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TOTHER INFORMATION: Anote= "start and stop positions for OTHER INFORMATION: cDNA containing a combination of both OTHER INFORMATION: 24d1 and 24d2 alleles
OTHER INFORMATION: (SEQ ID NO:12)"
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OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: qenomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
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OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                            8807-0088-998
                                                                        APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apy-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apy-1996
ATTORNEY/ABORT INFORMATION:
NAME: POISSAIL, Brian M.
REGISTRATION NUMBER: 28,462
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 89
TELECOMONIOLEATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFRAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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                                              PRIOR APPLICATION DATA:
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                                                4690 CACAAGTCATGGGTTTAATTTCTTTTTCTCCATGCATATGGCTCAAGGGAAGTGTCTATG 4749
                                                                                                                                                                           61 TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
                                                                                           121 CACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATG 180
                             TGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTATGAGACAGC 120
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APPLICANT: Sawada-Hirai, Ritsuko
APPLICANT: Barton, James C.
TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
FILE REFERENCE: 10653/002001
CURRENT APPLICATION NUMBER: US/09/277,457
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/09277457 Patent No. 6355425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-277-457-27
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12146
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Length 10825;

1 GGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTCTCCCAAATTC 60

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Query Match 100.0%; Score 301; DB 4; Best Local Similarity 100.0%; Pred. No. 6.6e-86; Matches 301; Conservative 0; Mismatches 0;

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Db 197113 AATGTCAAGGCCGGGCACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGAGG 197172
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Deter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: TWO Embarcadero Center, 8th Floor
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: FILES, Renee A.

REGISTRATION NUMBER: 35,136

REGISTRATION NUMBER: 35,136

REDEDIAMICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAM: 415-576-0200
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100.0%; Score 301; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.5e-85;
Matches 301; Conservative 0; Mismatches 0;
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LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                            ; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TVPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                       John N.
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US-08-724-394A-21
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                                                                                                                                                                                                       APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Woger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
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APPLICATION NUMBER: US/08/724,394A
FILING DATE: U1-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FILLS, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 301; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.5e-85;
Matches 301; Conservative 0; Mismatches 0;
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; LCGATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
          5-08-724-394A-20
Sequence 20, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 415-576-0200
TELEPAX: 415-576-0300
INFORMATION FOR SEQ ID NO. 20:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: not relevant
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APPLICANT: Kronmal, Gregory
APPLICANT: Lauer, Peter M.
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TYPE: nucleic acid
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Ruddy, David A.
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Sequence 7, Application US/09497957
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US-09-497-957-11 Sec

US-09-497-957-12 Sec

US-09-497-957-21 Sec

US-09-497-957-21 Sec

US-09-497-957-22 Sec

US-09-497-957-41 Sec

US-09-497-957-43 Sec

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US-09-497-957-7
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    Fast Pairwise Comparison

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The scores be Significance

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CTGCGTGAGTC CTGCGTGAGTC	510 TTGCGCTTGGG/ TTGCGCTTGGG/ 510	580 CGTCCAGACCCC IIIIIIIIII CGTCCAGACCCC 580	650 TCCCCGGCTG1 TCCCCGGCTG1 650	730 TAAATAAATCTC 	800 TTTCCAATGTCA !!!!!!!!!! TTTCCAATGTCA 800	870 AGAAGGCTGAGC AGAAGGCTGAGC 870	940 GGCGCGAAAGAG GGCGCGAAAGAG	1010 1020 GGTCTCTAGGGT GGTCTCTAGGGT	1090 GCCTGGAAATT GCCTGGAAATT	1160 GATTTGCAATGT GATTGCAATGT	1230 CACTTCTAAGTT CACTTCTAAGTT	1300 133 CGTTTATTTAC

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AAACAAGTA	2230
TGAAAAAAT	2220
SAAGCTCGGGT	2210
rcciggitaa	2200
STAGACAAAC	2190
ATGTCACCTA	2180
AAACTTTGCCAC	2170

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3	3160 CAGGAGTT	3230 316GTGGC 1111111 31330	3300 CAGGTTGC CAGGTTGC	70 AAAAAAA AAAAAAA	34 NACTCCT NACTCCT 34	3520 IGTCTAATC	3590 CACACAA(
3080	3150 TTGAGGTC TTGAGGTC	3220 'AGCCTGGTC 'AGCCTGGTC	SGAGGTGG	3370 ICAAAAAAA IIIIIIII ICAAAAAAA	3440 346CACC 1111111 3AGCACC 3440	3510 IGGAGIC: IGGAGIC: 3510	3580 GAGAAAAG
3070	3140 GTAGATCATI GTAGATCATI	AAAATTAC	3290 GAACCCAGG 	3360 CTCTGTC1 	3430 TTGCCCTC 	3500 CAGCTTTAG: CAGCTTTAG: 3500	GTGGCAG
	3140 3GCAGGTAG 3GCAGGTAG	3210 AAATACAA 	3280 ATCCCTT 	3350 GAGTGAGA GAGTGAGA	O STCTAAT STCTAAT	35 TCCACCA TCCACCA	3570 GCCACGT
3060	3130 TGGCTGAC TGGCTGAC	3200 CTACTAA! 	3270 GGTAGGAGA GGTAGGAGA	3: GTGATAG; GTGATAG;	3420 GATTTGGGT GATTTGGG	3490 TCTAGAA TCTAGAA 3490	3560 GGTGGCA
3050	3120 CACTTTGG' CACTTTGG' 3120	OCCATGT	3270 GCTTAGGTA GCTTAGGTA 3270	3340 AGCCTGG(AGCCTGG(3340	3410 TCCTCAG TCCTCAG	3480 TAACATTT TAACATTT	GTGAGGG
10	TCCCAGC	3190 STGAAACCC STGAAACCC	3260 TCAGGAG TCAGGAG	3330 GCACTCC 	3400 AGGAATTAT AGGAATTAT	ACACCIT	3550 GGGGGCAG
3040	3110 CCTGTAA CCTGTAA	3180 CAACATGO CAACATGO	3250 CCAGGTTT CCAGGTTT	reccact	3400 ACTGAAGGA ACTGAAGGA 3400	3470 SCTAGACA SCTAGACA	3540 AGGATCT
3030	3100 GCTCACTT GCTCACTT	3170 GCTTGGCC GCTTGGCC	3; ATAGTCCC ATAGTCCC	3320 GAGATTGTG GAGATTGTG	3390 AAAAAAAA AAAAAAAA	3460 TACCATGO TACCATGO	3530 TTGGAAT
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| 3610 | 3620 | 3630 | 3640 | 3650 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3670 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 | 3770 |

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3970 3980 4000 4010 4020 4030 AGGGTGGGATCACATGTTCACTTCTGGACTATTATGGAAAATCACAACCAGCAAGGGTATGTG	4090 4100 3CATCTTGAAGGAAACAGC 111111111111111111111111111111111111	06-60	4180 4190 4200 4210 4220 6GFGGAAATAGGGGCCTGGGGGGGGGGTTTTTCCAGGGCCCACCCTGGGGGGGATTTTTCCAGGGCCCACCCTGGGTGGG	4250 4260 4270 4280 4290 4300 4310 4320 CAGGTCATCCTGGGCTGTGAAATGCAAGAACAACAGTAACCGAGGGCTACTGGAAGTACGGGTATGATGGG	4330 4340 4350 4350 CAGGACCACCACCACCACCACCACCACCACCACCACCACC	4400 4410 4420 4430 4440 4450 4460 CTGGAGTGGGAAAGGGCCAAAGGGACTGCCCACAGGGACTGCCACAGGGACTGCAAAGGCACTGCAAAGGCAAAGGTGGAAAGGCAAAGGTGGCAAAGGAAGG	4470 4480 4490 4500 4510 4520 4530 CTGCAGCAGTGGTGGAACACACTTTTGGACCAACAAAGGTATGGGAAACACATTTTGCCCC TILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	4540 4550 4560 4570 4580 4590 4600 TATACTCTAGTGGCAGAGTGCAGGGCACGGAATCCCTGGTTGGAGTTCAGAGGTGCTGAG	4610 4620 4630 4640 4650 4660 4670 4680 GCTGTGTGCCTCTCCCAAATTCTGGGAAGGGACTTTCTCAATCCTAAGAGTCTCTAATAATTGAAATGTA [4690 4700 4710 4720 4730 4740 4750 TGAGACGCACAAGTCATGGGTTAATTTCTTTCTCCATGCATATGGCTCAAAGGGAAGTGTCTATGGCC	4760 4770 4780 4790 4800 4810 4820 CITGCTITTATAACCAATAALCITITGTATATTAACCGGTGTTAAAAATTCCAGAAAGCCGGG

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| 100 | 2820 | 2830 | 2840 | 2850 | 2860 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2870 | 2870 | 2870 | 2870 | 2870 | 2870 | 2870 | 2870 | 2870 | 2870 | 2870 | 2870 | 2870 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2870 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2880 | 2 CTCGGGGGCTGAGGTGGAGGTATTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCA 2740 2750 2760 2770 2780 2790 2800 CTCGGGAGGCTGAGGTGGAGGGTATTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCA 2890 2900 2910 2950 2930 2940 2950 297TTTTTTTTTTTTTGCCTGAGGGGGGGGGTAATTGGCAATGCGATTCTGAGATGGT

4330 4340 4350 4360 4370 4380 4390 4440 4450 4440 4446 CTGGAGTGGGAAAGGCACAGAGTTCGGCCAGCCAGACAGA	CTGCACCAGTTGCTGGAAGGTGTTTTGAACCAAAAGGTTGTTGGAAGGTTTTGCACCAACAAGGTTTTGTGTGGAAGGTTGTTTGGAAGGTTTTGGAAGGTTGTT	4610 4620 4630 4700 4720 4720 4720 4780 4780 4780 4780 4780 4780 4780 478	4830 4810 4810 4810 CACGGTGCCTCACCCTGTAATCCCAGCATTTGGGAGGCGGGGTGGTCACAAGGTTTGA	4970 4980 4990 5000 5010 5020 5030 5040 CCTGTAGTCCCAGGAAGTTGCACTGAGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	5120 5130 5140 5150 5160 5170 5180 AAAAAGAGAATTCAGGAATCTCAGCTATCATATGAATACCAGGACAAATATCAGTGAGCCCATTATCAG
TACCATGGCTAGACACCTTAACATTTCTAGAATCCACCAGCTTTAGTGGAGTCTGTCT		TGTEGCTCTGTCTCCAGGTTCACACTCTCGCACTACCTCATCATGGGTGCCTCACAGGCACCTTGGTCT 3750 3750 3750 3860 3810 3860 3870 3870 3870 3880 3870 3880 TTCCTTGTTGAAGCTTTGGGTACGTGGATGCCGTGTTCTTCTATGATNATGAGAGTCGCCGTGT 11111111111111111111111111111	GGAGCCCGGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGTTGAGTCTGAAAGTCTGAAAGTCTGAAAGTCTGAAAGTCTGAAAGTCTGAAAGTCTGAAAGTCTGAAAGTCTGAAGTCTGAGTGTGGAGTCTGAGGTGTGAGTCTGAGGTGTGAGTCTGTGACTTCTGGACTTGTGGAAAATCACAACCACGAAGGGTATGTGTGTTTTTTTT		GGTGGAAATAGGGGCTATTCCTTTGGAGTTAACAAGGCTGGGGATTTTTCCAAAGTCCTGAAGTCTGGGGGATTTTTTCCAAAGTCCTGGGGATTTTTTCCAAAGTCTGGAGTGGGGGTGTGAGTCCTGGGGGGGG

ATCATIT 	5400 PACATGTG FACATGTG 5400	5470 AAAATGGT AAAATGGT 5470	5540 TGAAAGTT CGAAAGTT S540	10 TCCTTTG TCCTTTG TCCTTTG	CCCCCAG	5760 CGTATTG 	5830 ATATACG ATATACG	900 AGCCAGG 11 1 1 1 AGCCAGG	0 GATCTGC 111111 GATCTGC 0	CCCTCAC	6120 GGAATT GGAATTT 6120
5260 5270 5280 5290 5300 5310 5320 CAAGTCCGCTTCTTATAACAATGCCTCCTAGGTTCACCCAGGTGAAACTCACCATTTT [30 5340 5350 5360 5370 5380 5400 CAATGCACATAAGGCCAATTTATCTATCAGAACAAGAACAGGTAACAGATATGTATTACATGTG CAATGCACATAAAGGCCAATTTTATCTATCAGAACAAGAACATGTGTATATTTATT	5410 5420 5430 5440 5450 5460 5460 5470 AGGAGAACAAGCTGATCTGCAAGTGACACTGTGTTAGAGTCCAATCTTAGGACACAAAAGG	5480 5530 5540 GTCTCTCTGTAGCTTGTTTTTTTGTGAAAGGGTATTTCCTTCC	5550 5560 5570 5580 5590 5600 5610	5620 5630 5680 5690 5690 5690 5690 5690 5690 5690 5690 5690 5690 5690 5690 5690 5690 5690 5690 5680 5680 5680 5680	5740 5750 CCAAGGAGTTGAAAGA 	5810 5820 TACCCCTGGGGAAGAGCAGAG TACCCCTGGGGAAGAGCAGAG 5810 5820	5880 5890 581 TCTGGGGTATGTGACTGATGAG 	5910 5920 5930 5940 5950 5960 5970 5960 5970 5960 5970 5960 5970 5960 5970 5970 5970 5970 5970 5970 5970 597	0 6030 6040 ACTTGCTTTTCTGTTTTAGAG ACTTGCTTTTTCTGTTTTAGAG ACTTGCTTTTTAGAG	6110 6110 ITTGTCGTCATCTTGTTCATT
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5260 5270 5 CAAGTCCGCTTCTTATAACAA' 	330 5340 5351 CAATGCACATAAAGGGCAATT 	5410 5420 AGGAGAACAGCTGATCTGAC	5480 GTCTCTCTGTAGCTTCTTTTT 	5550 5560 CCAGTCTTCCTCGCAAGGTA/ 	5620 5630 56 GTGAAGGTGACACATCATGTGA 	690 5700 5720 5730 5740 5750 AACATCACCATGAAGTGAAAGGATAAAGCAGCCAATGGATGCCAAGGAGCTACGAACCTAAAGACGTATTG	5770 5820 5830 5830 5830 5820 5830 5830 5830 5830 5830 5830 5830 583	5840 5850 5900 TNCAGGTGGAGCACCAGGCCTGGATCAGCCCTCATTGTGATCTGGGGTATGTGATGTGATGTGACGCAGG 5900 TILLILILILILILILILILILILILILILILILILILI	5910 5920 5930 5940 5950 5950 5970 AGCTCAGAAAATCTATTGGGGGTTGAGAGGGGCCTGAGGGGGTAATTATGGCAGTGACATGCGGGTTGCTGCTGTATTGTTGTTTTTTTT	5980 5090 6010 6020 6030 6040 TCTTTGTTTTTTTTTTTTTTTTAGAGCCCTCAC IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	6050 6060 6070 6080 6090 6100 6110 6120

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T GAAATCCA ATAGTGCCCAGGTCTAAATTGAGATGGGTGAATGAGAAAATAAGGAAGAAGAGAAGA		TGAAATCCAATAGTGCCCAGGTCTAAATTGAGATGGGTGAATGAGGAAAATAAGGAAGAGAGAAGA	7050
AATAAGGAAGA		AATAAGGAAGA	7040
TGAATGAGGAA		TGAATGAGGAA	7030
TTGAGATGGG		TTGAGATGGG	7020
CCAGGTCTAAA		CCAGGTCTAAA	7010
CCAATAGTGC		CCAATAGIGC	1000
TGAAAT	=	TGAAAT	0669

| 7490 | 7500 | 7510 | 7520 | 7530 | 7540 | 7550 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 | 7560 |

| 8210 | 8220 | 8230 | 8240 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 | 8250 |

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10580	GAAAAGCCCCTGAAAATTTGAGAAAACAAGAAACTACTTACCAGCTATTTGAATTGCTGGAATCACAG	GAAAAGCCCCTGAAAATTTGAGAAAACAAAACAAAACTACTTACCAGCTATTTGAATTGCTGGAATCACAG	10580
10570	ATTIGAATIG	ATTTGAATTG	10570
10560	CTTACCAGCT	CTTACCAGCT	10550 10560
10550	CAAGAAACTA	CAAGAAACTA	10550
10540	AGAAAACAAA	AGAAAACAAA	10530 10540
10530	GAAAATTTG	GAAAATTTG	10530
10520	GAAAAGCCCC	GAAAAGCCCCT	10520

10660 10660

10730 10730

10820

US-09-497-957-1 (1-10825) US-09-497-957-3 Sequence 3, Application US/09497957

4.02 Optimized Score = 10825 Significance Matches = 10823 Mismatches Conservative Substitutions 10825 998 0 . . . Initial Score Residue Identity Gaps ### 120 | 120 | 140 | 140 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 15

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	턴트턴	g – g	8-8	01-10 01-10	ra – ra	9-9	5 – 5 5 – 5	8 - 8 8 - 8	0
430	440 450 450 500 CTGCGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	510 520 570 TTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGCTCAACCCCAACCCCACCTACTTCTG TTGCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGCTTAACCTATCCGCAAGCCCCTACTTCTG TTGCGCTTGGGAACTTTGGTAACTTTGGAGGACCTGCTCAACCGCAACCGCAACCGCAACTTGGTAACTTTTCTGTAACCTTTTTTTT	580 60 610 620 630 640 CGTCCAGACCCGTGAGGGGTCCTACCCCTACGCCCCCAGGACTGCCCCC 111111111111111111111111111111111111	50 660 710 720	730 770 780 790 750 750 750 770 770 770 770 790 790 790 790 790 79	800 840 850 860 800 800 800 840 850 860 860 810 850 860 860 860 860 860 860 860 860 860 86	#70 #80 #80 #80 #90 #90 #90 #90 #90 #90 #90 #90 #90 #9	940 GGCGCGAAAGAGTGGCGTTGGGGATCTGAATTCTTCACCATTCCACCCAC	1080
•	500 CTTT 1111 CTTT	570 TACT TACT 570	CTG	SAAT	2000 1111 2000	860 FGCTT FGCTT 860	930 GGCG GGCG 930	0 TGGG TGGG	
	CTAG	2007	640 GGAC(GGAC(640	10 CTAC CTAC CTAC	AAC:	GAG GAG	1116 1116	1000 ACCT (111	0.50
420	0 AAA(TCT HEL	CCA A	CCAA	780 2166 1111 780	850 TCCCT 11111 TCCCT 850	raca 	rgag rgag	,
	490 ATCGA/ ATCGA/	560 560 560	0 - 0 0	3 = 3 3 = 3 3 = 3	AACC	CTTC	920 GAA7 GAA7	11GG	
_	AAA AAA	AAG 	630 SCCTCC 11111 SCCTCC 630	700 1011 1011	01110 01110	AGTT AGTT	GAAC	990 CTTTT 	0 9 0 1
410	480 GTGGP GTGGP	0500	6610 	1,01-0 1,1-0 1,1-0	770 CTCC7 1111 CTCC7	840 AGGA 1111 AGGA 840	TCA	CCA	-
	4 3666 1111 3666	550 CIAI CIAI 550	620 ATAGG ATAGG 620	- CCCA	3666 111 3666	AACA AACA B	910 CACC CACC 910	980 TCCAC TCCAC 980	
0) 	ACC	6. 111 111 868	069 1 - 1 - 1 069 069	760 AGCCT 1111 AGCCT 760	CCA CCA	1111 	SATT	0
400	470 CGCG 1111 CGCG	CTCA	CTGC	GGA4 GGA4	76 TAAC TAAC	830 ATC:	0 66667 111	CAC	
	00000	540 301603 11111 301603 540	610 TGAA TGAA 610	CTTT FITT	3AGC 1111 3AGC	AGTC - - AGTC	900 CACGGC CACGGC 900	970 TCT1 TCT1 970	
390	CTAG	GGAC	CACT	68(GACT GACT 68(750 AGCT(AGCT(750	0000	9000 111 9000	SAAT	,
e.	460 2GAA(1111 2GAA(460	530 TTGGA TTGGA 530	CTAC	GAGT	TTGP TTGP	820 TTTC TTTC TTTCC 820	890 AGGA1 AGGA1 890	TCT(
	09999	SCITION SE	600 116CC 111 600	70 16CG 1111	ICAC IIII	STTT	AGCA AGCA AGCA 8	960 366A 1111 366A	,
380	CTGC	CTAA	GGAG	CTC1	740 TCCJ TCCJ 740	O GCAC GCAC	CAC	111G(111	•
•	450 GGGCT GGGCT 450	.520 GTTTG 520	rgag rgag	5000	ragt ragt	810 CTGTG(CTGTG(810	880 AACC AACC 880	00000	
	2003 0003	GAGT	590 CCGT(CCGT(590	60 GTC(GTC(61	11CG	CAG 	GCA HGCA	95 SAGT 1111 SAGT 95	
370	40 GAGT 1111 GAGT 40	1766 1111	3ACC 3ACC 3ACC	9 36CT 36CT 6	730 AATC AATC 730	800 AATGI 1111 AATGI 800	CTG# CTG#	AAAC AAAC	
	CGTC	510 CGC CGC 510	80 TCCA(1111 TCCA(80) - - 	ATA NATA	8 CCA 8 8	870 VAGG(1 1	2000 1000 1000 1000 1000	
	CTG - - CTG	71G 	58 CGT 111 CGT	650 TCC 110 TCC 650	TAP TAP	TT- 	AGI AGI	9 9 – 9 9	

	1510 2320	2450 2460 2540	1800 2610	1840 2750 1840 2750 CTCGGAGCTGAGCTGAG ACTCGGAG	2810 2820 28 28 28 28 28 28 28 28 28 28 28 28 28		2160 2970 TGTCTCT 11111111111111111111111111111111
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6580	GGATCTTGA	rggarcttga 6580	6650
6570	PGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGGAGCTGGATTCCATTAGGTGAGGTTGAAGATGATGGG	FGGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCATTAGGTGAGGTTGAAGATGATGGG 6560 6570 6580 6590 6620	6630 6640 6650 6660 6670 6680 6690
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4. US,09-497-957-1 (1-10825) US-09-497-957-1 Sequence 1, Application US/09497957

4.02 2 0 500 210 Significance Mismatches 490 200 Optimized Score = 10825 Matches = 10823 Conservative Substitutions 480 190 470 180 460 170 0 866 450 160 Score Identity 440 Initial s Residue 1 Gaps

us-09-497-957-1.res

1660 1670 1680 1690 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 CTGTTCAAGCCCAAGGGGAAACAAGTCTTTACCCTTTGATTTTGCATTCTTGGGAA	1810 1820 1830 1840 1850 1860 1870 GATGACAATAGCAAAGAATATACAACATCAGGAAATCATGGGTGTTGTGAGAAGCAGAAGGGGGGGG	1880	1950 1960 2010 CAGTATITCCAGGCAACTGAGTGGCAACTGGATAAAAAGGGGGTTTCAGACACTAACTCAT	2020 2080 GGTGTGTGTGTGGGGGGGGGGGGGGGGGGGGGGGGG	2090 2100 2110 2120 2130 2140 2150 2160 GORGATACCTGTACTACTACTACTACTACTACTACTACTACTACTACTACT	2170 2180 2200 2210 AAACTTGCCACATGTCACTAGTAGACTCCTGGTTAAGAAGGTTGAAAAAAAA	2240 2250 2260 2270 2280 2290 2300 GTGCTGGGGGTGAGGGGCCTCAGAAGGGTCAGAGGTTGCAGGCG GGGGGGGGGG	2310 2320 2330 2340 2350 2360 2350 2370 2370 2370 2370 2370 2370 2370 237	2380 2440 GGTGCTATGGAAAGCAAGAGCAGACAGAAAGCAGGAGCAGGAGCCCAGCAG	2450 2460 2470 2480 2520 AGTCCAGGCAGAGGTAGGGTGGGGTGGGGAACAGGAAAGGGAGTACAAAACCATTGTCTCCTGAA	2530 2590 2590 2590 TATATTTGAAGGAAGGAAGGAAGGAAGAAGAAGAAGAAGA
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                                                                                                                                             9590
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                                                                                                                                             9580
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9800 9810 9820 9830 9840 9850 9860 TACTTAAN GETTTTGCCATAGGGAATA INTEGRATA AND GARATTTGCTTTAGGGAATA INTEGRATA ATTTGCTTTAAN TITTGCTTTAAN GAATA TAGGAATA TAGGAATA TAGGAATA TAGGAATA TAGGAATA TAGAGAATA TAGATATTGCTTAAN TAGATATTGCTTAAN TAGATATTGCTTAAN GAATA TAGATATTGCTTAAN GAATA TAGATATTGCTTAAN GAATA S800 9810 9820 9880

CGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAAGAATGGGTGGAGGGGCGTGCACTGGAAATCACTTGTAGA

10480

10470

10460

10450

10510

10500

10490

| 10590 | 10600 | 10610 | 10620 | 10630 | 10640 | 10650 | 10590 | 10590 | 10600 | 10600 | 10720 | 10690 | 10720 | 10720 | 10720 | 10690 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 10720 | 1072

. US-09-497-957-1 (1-10825) US-09-497-957-9 Sequence 9, Application US/09497957 Initial Score - 677 Optimized Score - 786 Significance - 0.00 Residue Identity = 58% Matches - 895 Mismatches - 470 Gaps - 167 Conservative Substitutions - 0

1280 1290 1300 1310 1320 1330 1340 13666GTAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1360	420 1450 1450 1450 1450 1450 1450 1450 145	1480 1500 1510 1520 1540 1560	1550 1560 1570 1580 x 1610 1620	1630 1640 1650 1660 1670 1680 1690 TATGATTCTTAAACATCACACTGCATTAGAGGTTGAATAATAAATTTCATGAGCAGAAATATTCATTG	5-09-497-957-1 (1-10825) 5-09-497-957-11 Sequence 11, Applica lal Score = 676 Optimized Sco Tue Identity = 58% Matches	Gaps	AACACCCCTTCAGGATTTAAAACCAAGGGGGACACTGGATCACCTAGTGTTTCACAAGGAGGTACCTTCTG	CTGTAGGAGAGAACTAAAGTTCTGAAAGACTGTTGCTTTTCACCAGGAAGTTTTACTGGGCATCTCC	TAGCTGTAGGGTGACTTCTGGAGCCATCCCCGTTTCCCCGCCCCCCATING	340 350 350 350 350 350 350 350 350 350 35	400 410 420 430 440 450 460 470
0 290 300 310 90 500 510 520 5AAACTAGCTTTTCTTTGGGGAG-TTGCTAACT 	S40 S50 S50 S60 S60	610 620 630 640 650 660 670 CT-GAACTGC-AGATAGGGGTCCTCGCCCAGGGTCCCCGGCTCTCCGGGTCTGCGGAG-	680 740 740 740 740 740 740 740 740 740 74	750 760 800 810 CT-TGACCTGACCTAGACCTCTTGAACCTGGAACT-CGGGT-TTATTTCCAATGTCAGCTGTG [#20 #30 #40 #50 #50 #60 #70 #70 #60 #70 #70 #70 #70 #70 #70 #70 #70 #70 #7	880 890 930 920 930 930 920 930 930 930 930 930 930 930 930 930 93	940 950 1000 1010 CGGAAAGAGGGGTGGGGATCTGAAACATTCTCACCCACTTTTGGTGAACGGGGGGGG	1020 1030 1040 1050 1050 1060 1070 TCTC-TAGGGTGGGAGGTCTCTGAGAGAGGCCTACCTGGGGCCTTTCCCCACTCTTGGCAATTG	1080 1090 1100 1110 1120 1120 1140 TTCTTTIGCCTGGAAAATTAAGTATATGTTAGTTTGAACGTTTGAACTGAAC	1150 1160 1170 1180 1190 1200 CTAGGCTTATATGATTGCAATGTGCTGTGAATTAAGAGCCTCTTACAAGTACTGATAATGAACA	1220 1230 1240 1250 1260 1260 1270 1270 1270 1270 1270 1270 1270 127	1070 1080 1090 1100 1110 1120 1130

| 820 | 830 | 840 | 850 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870

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7. US-09-497-957-1 (1-10825) US-09-497-957-10 Sequence 10, Application US/09497957 Initial Score = 676 Optimized Score = 786 Significance = -0.00 Residue Identity = 58% Matches = 899 Mismatches = 463 Gaps = 173 Conservative Substitutions = 0

1210 1220 1230 1240 1250 1260 1270 AACATGTAAGCAATGCACTCAAGTTACATTCATATTGATTTTCACT-AGGCACATCAATCTAATTTGATTTTCACT-AGGCACACAGCAGCACCCGGCCTGGATCGGGATCGGGACCCTCACGCTCGGACCCTCACGCTCGGACCCTTCACGTTTGATCTGGATCGGGACCCTTCGACTCGGACCCTTTGATTTTACTAGAATTCAGAATTCAGAATAATAATAATATTTTACTAGAAGTTAACTGCAATTAATATAATAACTCTTTTACTAGAAGTTAAATAACTCTTTTACTAGAAGTTAAATAACTCTTTTACTAGAAGTTAAATAACTCTTTTACTAGAAGTTAAATAACTCTTTTACTAGAAGTAACTGGAATTAATAAAATTTTACTAGAAGTTAACTGCTCATTG-TTC-ATTGGAATTTTACTTACTACAACTTG-TTCATTGGAATTTTACTAGAATTTTACTAGAATTTTACTAGAATTTTACTAGAATTTTACTACAATTTACTAGAATTTACTAGAATTTTACTAGAATTTACTAGAATTTACTAGAATTTTATTTTATTTA	1150	1480	8. US-09-497-957-1 (1-10825) US-09-497-957-12 Sequence 12, Application US/09497957 Initial Score	190 200 210 220 230 240 250
190 200 210 220 230 240 250 260 260 400 410 420 430 440 450 460 470	TCATGGCTGCTCAGAGCAGGACCTTGGTCTTGTTTGAAGGTTTGGGCTACGTGGATGACCA 330 340 550 560 570 580 600 600 600 600 600 600 60	680 TGACTTTGGAACCGCCCACTCCCCAACTAGAATGCTTTAAATAAATCCGTAGTTCCTCA TGACTTTTGGAACCGCCCACTCCCTTCCCCAACTAGAATGCTTTTAAATAAA	880 890 700 710 720	860 870 880 890 910 920 920 910 920 920 1080 1180 1180 1140 1120 1130 1140 1140 1120 1130 1140 1140 1170 118

| 820 | 830 | 840 | 850 | 870 | 860 | 870 | 870 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871 | 871

 LOYU TIGTITA 9. US-09-497-957-1 (1-10825) US-09-497-957-21 Sequence 21, Application US/09497957 Initial Score = 516 Optimized Score = 516 Significance = -0.07 Residue Identity = 99% Matches = 516 Mismatches = 1 Gaps = 0 Conservative Substitutions = 0

us-09-497-957-1.res

GGGGATGGGACCTACCAGGGCTGGP	5840 5850 5860 GTGGAGCACCCAGCCTGGATCAGC 	20 ATTGGGG ATTGGGG	\$990 TTAGGGGTGGCTGAGGTGGC TTAGGGTGGCTGAGGTGCCAT	480 490 500 6060 6070 608 GCACCCTAGTCATTGGAGTCATCAC	11. US-09-497-957-1 (1-10825) US-09-497-957-42 Sequence Initial Score = 39 Og Residue Identity = 97% MG Gaps = 0 CC	3760 3770 CTGTCTCCAGGTTCACACTCTGG	3830 3840 36 TTTGAAGCTTTGGGCTACGTGGAT	3900 3910 3920	CGAACICCAIGGGTTICCAGTAGA	GATCACATGLTCACTGTTGACTTC 12. US-09-497-957-1 (1-10825-05-09-497-957-41 Sequence	Initial Score = 39 Op Residue Identity = 97% M Gaps 3760 3770	3830 TTTGAAGCTTTGGGCTACGTGGAT	3900 3910 3920 CGAACTCCATGGGTTTCCAGTAGA: 3970 3980 3990 GATCACATGTTCACTGTTGACTTC	13. US-09-497-957-1 (1-10825 US-09-497-957-30 Sequence
120 130 140 150 160 170 180	5700 5750 5760 ACCATGAAGTGGATAGCACCAATGGATGCCAAGGAGTTGGACCTAATGGACCCAATGCCCAATGCCCAATGCCCAATGCAAGGACTAAGGACGAATTGCCCAATGATTGCCCAATGATTGCCCAATGATTGCCCAATGATTGCCCAATGATTGCAATGATTGCCCAATGATGATGATGATGATGCCAATGATGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATTGCCCAATGATGATGCCAAGGAGTTCGAACGTAAAGACGTATTGCCCAATTGCCCAATGATGATGATGATGATGATGATGATGATGATGATGATG	5770 5780 5810 5820 5830 GGGGATGGACTGGATRACCTTGGCTGRACCCCTGGGGAAAGCAGGAGAAATACGTNCCAG 111111111111111111111111111111111111	5840 5850 5860 5910 5810 6820 5810 6820 5910 6910 6910 6910 6910 6910 6910 6910 6	5920 5930 5940 5950 5960 5970 5980 5970	410 420 430 440 450 460 470 5990 6000 6010 6020 X 6030 6040 6050 TTAGGGGGTGGCTGAGGCATCAAAGGCTTTAACTTTTTTTT	6060 6070 6080 6090 6100 6110 6120 GCACCCTAGTCATIGGAGTCATCAGTGGAATTGTGTTTTTTTTTT	10. US-09-497-957-1 (1-10825) US-09-497-957-20 Sequence 20, Application US/09497957	Initial Score = 516 Optimized Score = 516 Significance = -0.07 Residue Identity = 99% Matches = 516 Mismatches = 1 Gaps 0 Conservative Substitutions = 0	5410 5420 5430 5440 5450 5460 5470 ACAAGCTGATCTCAAGTGACACTGTGTTAGAGTCCAAATCTTAGGACACAAAATGGTGTCTT	5480 5490 5500 5510 5520 5530 5540 5550 CCTGTAGCTTGTTTTTCTGAAAAGGGTATTTCCTCCCAACCTATAGAAGGAAG	0 5590 5610 CCCACATCTTCTTTGTGTAAGTGCCTCTTTG	5630 5640 5650 5650 5690 5690 5690 5690 678ACACATCTCAGTCACCACTCTCAGTCACCACTCTCAGTCACCACTCTCAGTCACCACTCTCAGTCACCACTCTCAGTCACCACTCTCAGTCACTCTCAGTCACTCTCACTCA	5700 5710 5720 5730 5740 5750 5760 ACCATGAAGTGGCTGAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAAT	5770 5780 5800 5820 5830 GGGGATGGGAACCTACCCTTGGCTGTACCCCCTGGGGAAGACAATATACGTNCCAG IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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3780 3790 3800 3810 3820
GCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTG
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AATTTCAAGCCAGTGCAGCTGCAGTCTGAAAGGGTGG
SATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACGTGCCAG
390 320 330
                                                                                                                                                                                      3780 3820 3820 3820 3810 3820 GCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 3930 3940 3950 3960
AATTICAAGCCAGATGIGGCTGCAGCTGAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimized Score = 39 Significance = -0.26
Matches = 39 Mismatches = 1
Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                    Optimized Score = 39 Significance = -0.26
Matches = 39 Mismatches = 1
Conservative Substitutions = 0
                                                                                                                                                                                                                                                                080 6090 6100 6110 6120
AGIGGAAITGCIGITITIGICGICAICTIGITCAITGGAAITITGI
                                                                                                                                                                                                                                                                                                                  5)
ce 42, Application US/09497957
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ce 41, Application US/09497957
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Matches
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3910 3920 3930 3940 3950 3960 3970 TGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGTGGGGATCACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3640 3650 3660 3670 3680 3690 3700 GACTGCAACTCACCATTCACAAATGAGGACCAGACACACGCTAATGATGCAGGTGTTGATGCAG
3770 3780 3830 3810 3820 3830 3810 3820 3830 3810 3820 3830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 310 X 320 330 x 340 350 CTGGAGCCATCCCCGTTTCCCCGCCCCCAAAGAAGAAGGAATTTAACGGGGACGTGCGGCCAGAGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 370 380 380 400 410 420 GAAATGGGCCCGCGGGGCGGCGCTCTCCTCCTGATGCTTTTGCAGACCGCGGTCCTGCAGGGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3780 3790 3800 3810 3820 3830 3840 GCACTACCTTGTTGAAGCTTTGGGGCTACGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3860 3870 3880 3890 3900 3910 3920 GTTCGTGTGTGTATACAAGTATTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 230 240 280 260 200 280 AGACCTGTTTTCACCAGGCAACTTTTACTGGGCATCTCCTGAGGCCTAGGCAATAGCTGTAGGGTGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial Score = 20 Optimized Score = 20 Significance = -0.26 Residue Identity = 100% Matches = 20 Mismatches = 0 Gaps = 0 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                       22 Optimized Score 22 Significance -0.26 100% Matches 22 Mismatches 0 Conservative Substitutions 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 Optimized Score = 20 Significance 100% Matches 20 Mismatches 0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19. US-09-497-957-1 (1-10825)
US-09-497-957-18 Sequence 18, Application US/09497957
                                                                                                                                                                                                                                                                                                                              US-09-497-957-1 (1-10825)
US-09-497-957-31 Sequence 31, Application US/09497957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18. US-09-497-957-1 (1-10825)
US-09-497-957-24 Sequence 24, Application US/09497957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAAAGAAGCGGAGATTTAACG
X
                                                                                                                                                                                                                                                                       PTCACTGTTGACTTCT
                                                                                                                                                                                                                                                                                                                                                                                    Initial Score Residue Identity Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial Score Residue Identity Gaps
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TIGCIG
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TGAC
                                                                                                                                                                                                                                                                                                                                  17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3770 3820 3830 3830 3820 3830 GGTICACACTCTGCACTTTCTTCTTGTTTGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3910 3920 3930 3940 3950 3960 3970 TGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTTGAAAGGGTGGGATCACATG
                                                                                                                                                                                                                                                                     5860 5870 5880 5890 5900 5910 5920 ATCAGCCCTCATTGTGATGATGACTGATGAAAATCTATTGGGGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5720 5730 5740 5750 5760 5770 5780 ATAAGCAGCCAATGGGATGCCAAGTACGAGCTAAAGACGTATTGCCCAATGGGGATGGGACCTAACAGG
                                                                                  Optimized Score = 30 Significance = -0.26 Matches = 30 Mismatches = 2 Conservative Substitutions = 0
    Optimized Score = 38 Significance = -0.26 Matches = 38 Mismatches = 1 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 Optimized Score = 38 Significance = -0.26
97% Matches = 38 Mismatches = 1
0 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 Optimized Score = 31 Significance = -0.26 96% Matches = 31 Mismatches = 1 0 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                          14. US-09-497-957-1 (1-10825)
    US-09-497-957-29 Sequence 29, Application US/09497957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16. US-09-497-957-1 (1-10825)
US-09-497-957-44 Sequence 44, Application US/09497957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15. US-09-497-957-1 (1-10825)
US-09-497-957-43 Sequence 43, Application US/09497957
                                                                                                                                                                                                                                                                                                                                5930 5940 5950
AGAGGAGTGCCTGAGGAGGTAAT
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AGAGGAGTGCCTGAGGAGGTAAT
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    Initial Score Residue Identity Gaps
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-0.26

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20. US-09-497-957-1 (1-10825) US-09-497-957-13 Sequence 13, Application US/09497957

Initial Score = 20 Optimized Score = 20 Significance = -0.26

Residue Identity = 100% Matches = 20 Mismatches = 0

Gaps = 0 Conservative Substitutions = 0

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